

Fig.1.

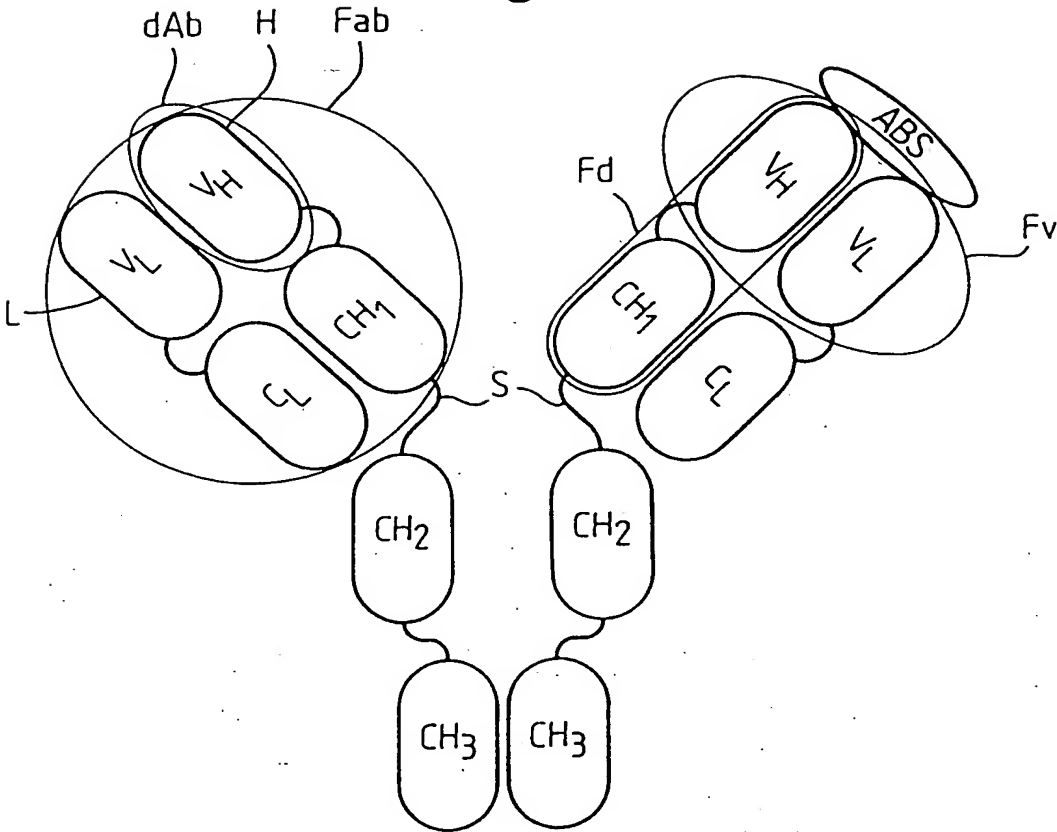


Fig.2 a

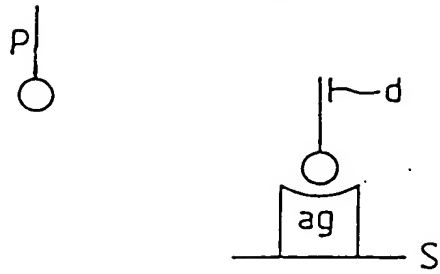


Fig.2 b

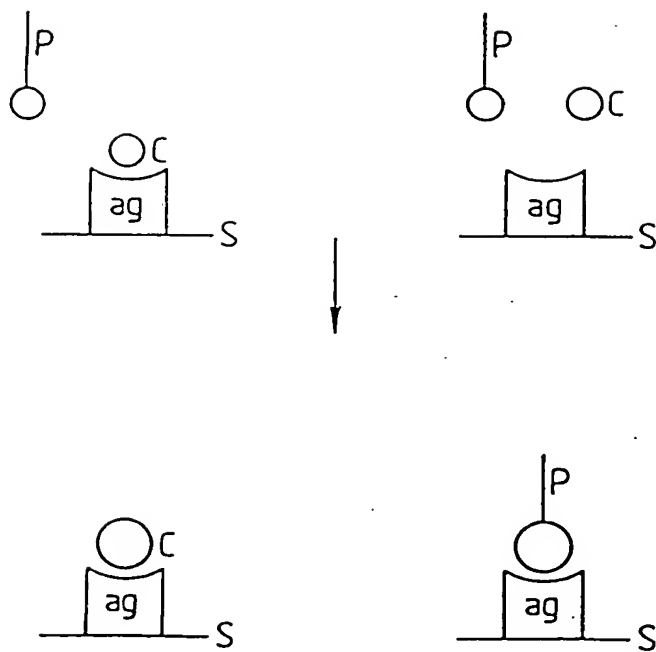


Fig.3.

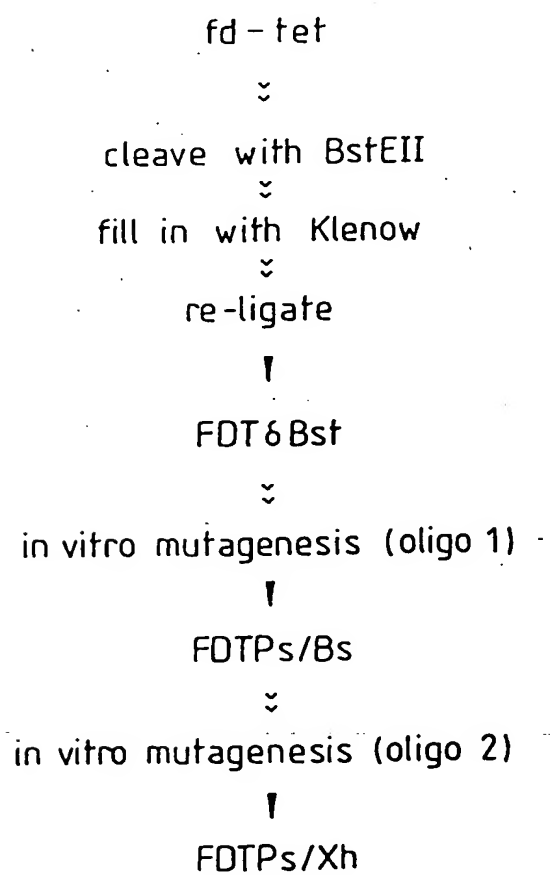
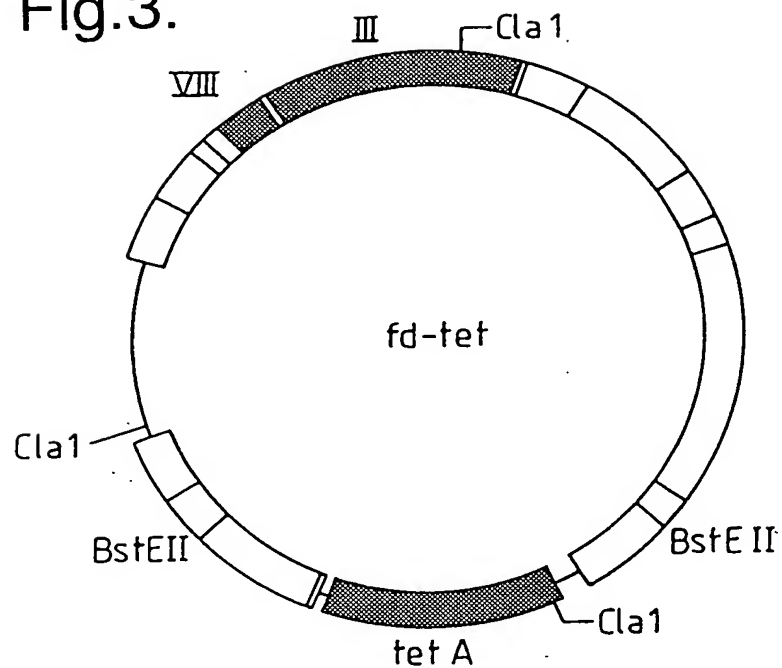


Fig.5a

rbs M K Y L L P T A A
 GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60
 SphI
 PelB leader
 A G L L L L A A O P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120
 PstI
 G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180
 S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTCGAGTGG
 190 200 210 220 230 240
 VHD1.3
 L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300
 S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360
 D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420
 Linker Peptide
 Q G T T V T V S S G G G G S G G G S G
 CAAGGCACCAACGGTCAACGTCTCCTCaggtggaggcggttcaggcgagggtggctcggc
 430 440 450 460 470 480
 BstEII
 G G G S D I E L T Q S P A S L S A S V G
 ggtggcggatcgGACATCGAGCTCACTCAGTCTCCAGCCTCCCTTTCTGCGTCTGTGGGA
 490 500 510 520 530 540
 SacI

Fig.5 b

E T V T I T C R A S G N I H N Y L A W Y
GAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTAT
550 560 570 580 590 600

Q Q K Q G K S P Q L L V Y Y T T T L A D
CAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATTATACAACAACCTTAGCAGAT
610 620 630 640 650 660

VKD1.3

G V P S R F S G S G S G T Q Y S L K I N
GGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
670 680 690 700 710 720

S L Q P E D F G S Y Y C Q H F W S T P R
AGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGGAGTACTCCTCGG
730 740 750 760 770 780

Myc Tag (TAG1)

T F G G G T K L E I K R E O K L I S E E
ACGTTTCGGTGGAGGGACCAAGCTCGAGATCAAACGGGAACAAAACTCATCTCAGAAGAG
790 800 810 820 830 840
XhoI

D L N * * (SEQ ID NO. 183)
GATCTGAATTAATAATGATCAAACGGTAATAAGGATCCAGCTCGAATTC (SEQ ID NO. 184)
850 860 870 880

EcoRI

Fig.6.

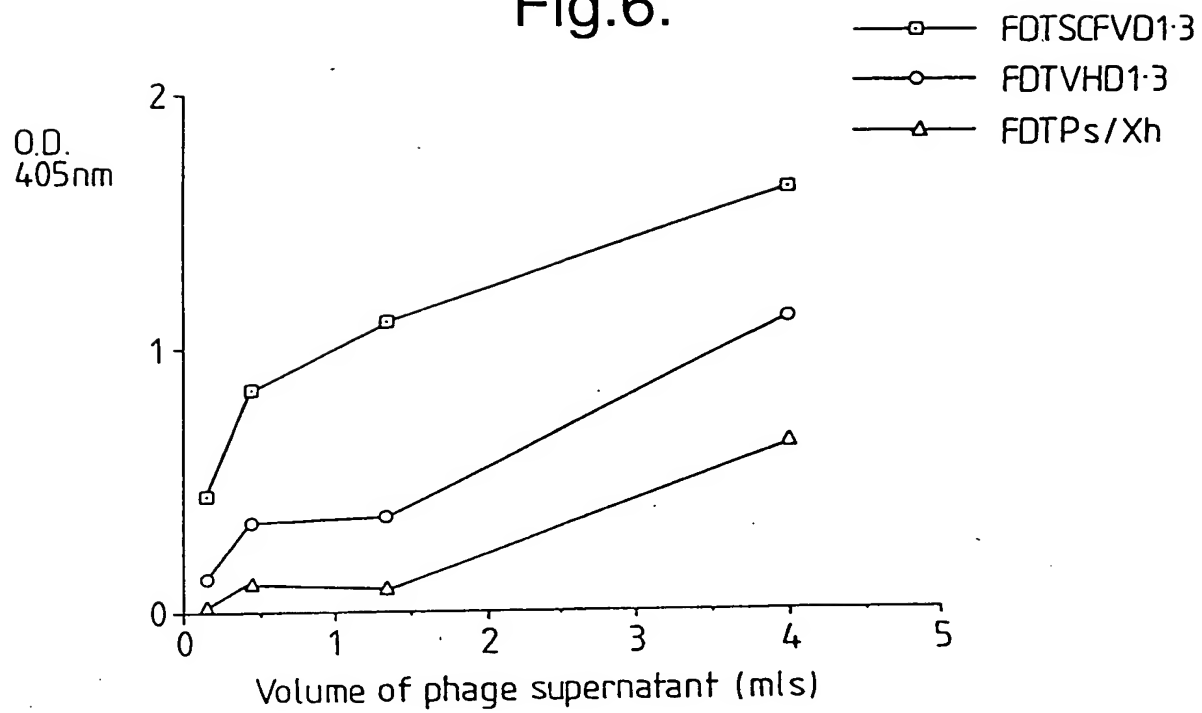


Fig.7.

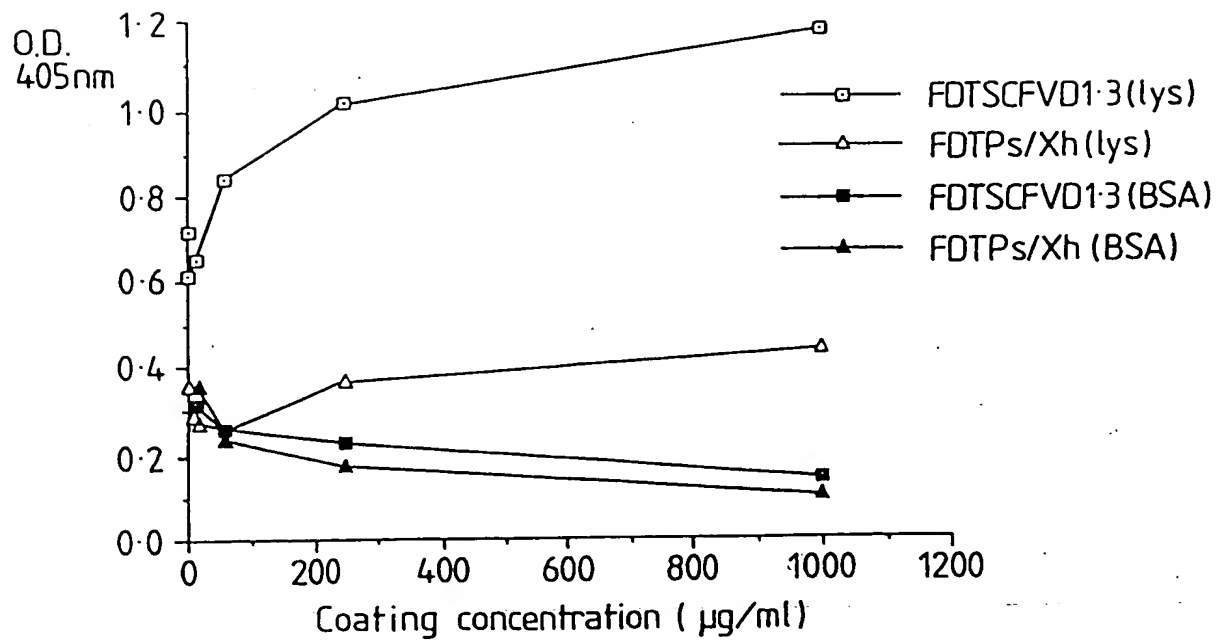


Fig.8.

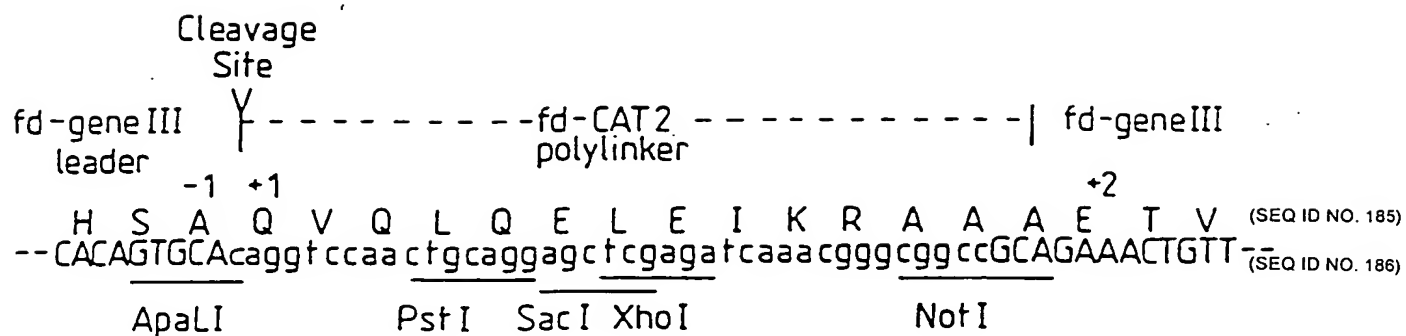


Fig.9.

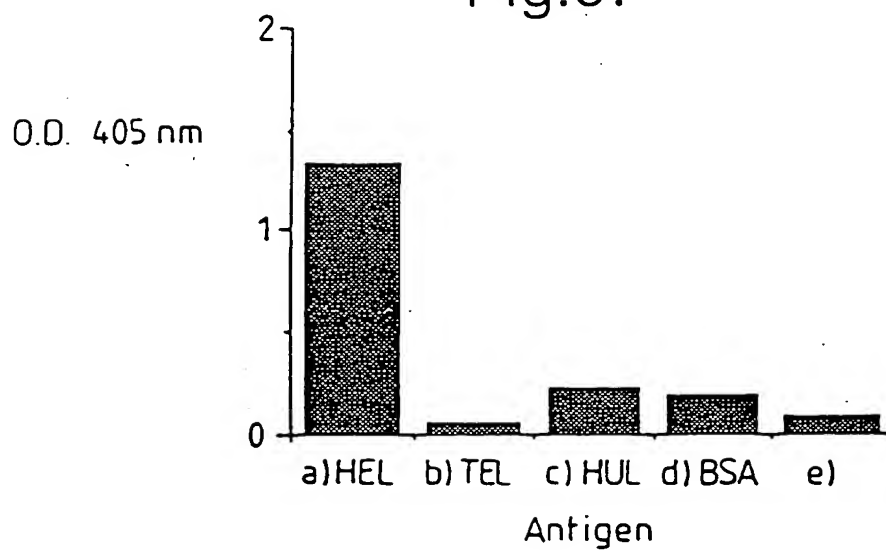


Fig.10a

M K Y L L P T A A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTAGGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTGCTGCCCAACCAGCGATGGCCCTGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCCTGGTGGGGCCCTCAGAGCCGTGCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTCGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S A S T K G P S V F P L
CAAGGCACCAAGGTACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
430 440 450 460 470 480

A P S S K S T S G G T A A L G C L V K D
GCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGCTGCCTGGTCAAGGAC
490 500 510 520 530 540

Fig.10b

Y F P E P V T V S W N S G A L T S G V H
TACTTCCCCGAACCGGTGACGGTGTGTGTGGAACCTCAGGCGCCCTGACCCAGCGGGGTGCAC
550 560 570 580 590 600

T F P A V L Q S S G L Y S L S S V V T V
ACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGGTGGTGACCGTG
610 620 630 640 650 660

P S S S L G T Q T Y I C N V N H K P S N
CCCTCCAGCAGCTTGGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
670 680 690 700 710 720

T K V D K K V E P K S S * * (SEQ ID NO. 187)
ACCAAGGTGCAACAAGAACTTGAGCCCAATCTTCATAATAACCCGGGAGCTTGCATGCA
730 740 750 760 770 780

M K Y L L P T A A A G L
AATTCTATTTCAGGAGACAGTGCATAATGAATACCTATTGCCCTACGGCAGCCGCTGGAT
790 800 810 820 830 840

L L L A A Q P A M A D I E L T Q S P A S
TGTTATTACTCGCTGCCCCAACCCAGCGATGGCCGACATCGAGCTCACCCAGTCTCCAGCCT
850 860 870 880 890 900

L S A S V G E T V T I T C R A S G N I H
CCCTTTCTGGTCTGTGCGAGAACTGTACCATCACATGTGCGAGCAAGTGGGAATATT
910 920 930 940 950 960

N Y L A W Y Q Q K Q G K S P Q L L V Y Y
ACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAATCTCCTCAGCTCCTGGTCTATT
970 980 990 1000 1010 1020

Fig.10 c

T T T L A D G V P S R F S G S G S G T Q
ATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACAC
1030 1040 1050 1060 1070 1080

Y S L K I N S L Q P E D F G S Y Y C Q H
AATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTTACTGTCAAC
1090 1100 1110 1120 1130 1140

F W S T P R T F G G G T K L E I K R T V
ATTTTGGGAGTACTCTCTGGACGTTGGTGGAGGCCACCAAGCTCGAGATCAAACGGACTG
1150 1160 1170 1180 1190 1200

A A P S V F I F P P S D E Q L K S G T A
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT
1210 1220 1230 1240 1250 1260

S V V C L L N N F Y P R E A K V Q W K V
CCTCTGTTGTGTGGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGGAAGG
1270 1280 1290 1300 1310 1320

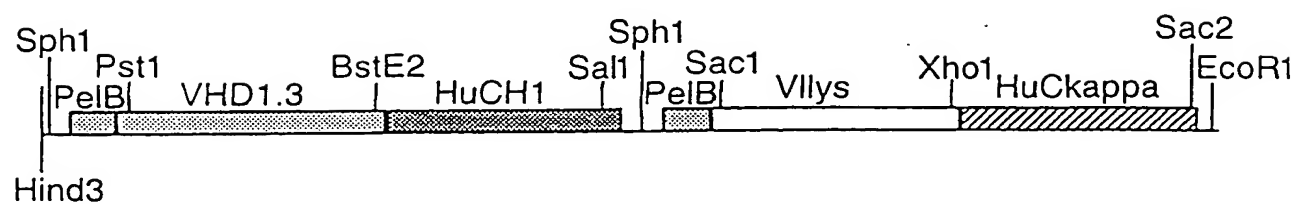
D N A L Q S G N S Q E S V T E Q D S K D
TGGATAAGGCCCTCCAATGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGG
1330 1340 1350 1360 1370 1380

S T Y S L S S T L T L S K A D Y E K H K
ACAGCACTACAGCCTCAGCAGCA.CCCTGACGCTGAGCAAGCAGACTACGAGAAACACA
1390 1400 1410 1420 1430 1440

V Y A C E V T H Q G L S S P V T K S F N
AAGTCTACGCTGCGAAGTCAACCATCAGGGCCTGAGCTGCGCGTCACAAAGAGCTTCA
1450 1460 1470 1480 1490 1500

R G E S * * (SEQ ID NO. 188)
ACCGCGGAGAGTCATAGTAAGAATTC (SEQ ID NO. 189)
1510 1520

Fig.10 d



FabD1.3 in pUC19

Fig.11.

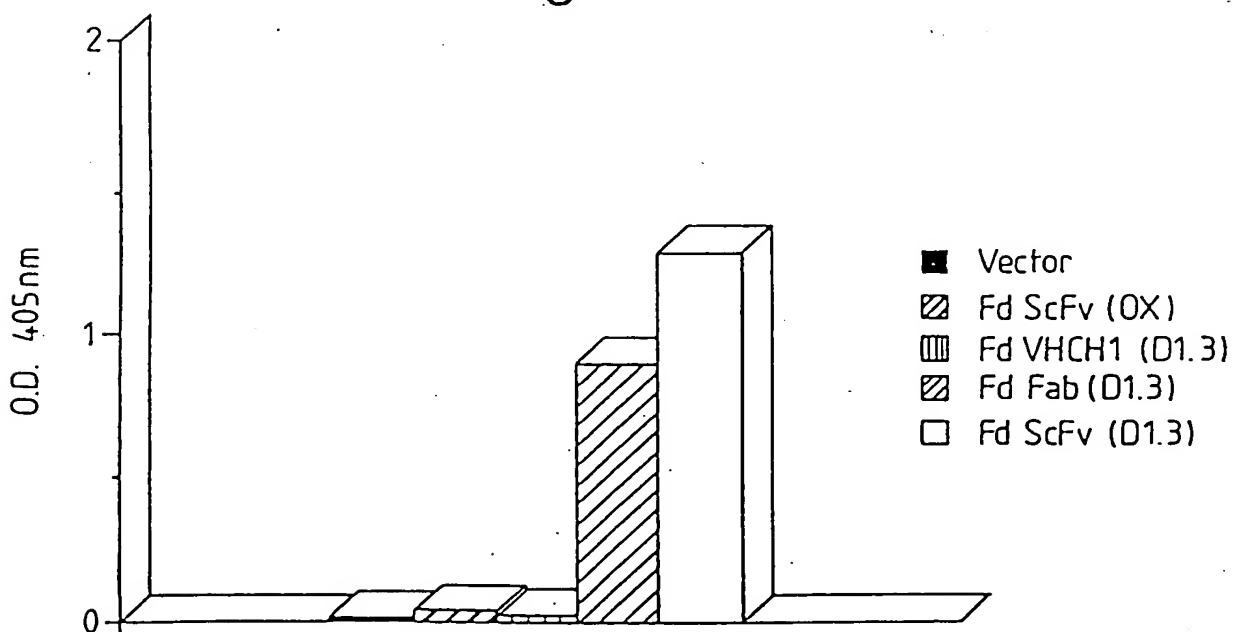


Fig.12a.

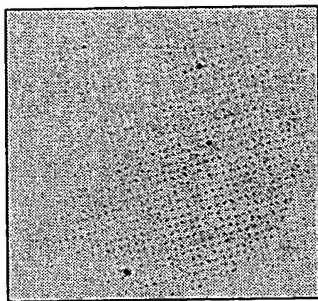


Fig.12b.

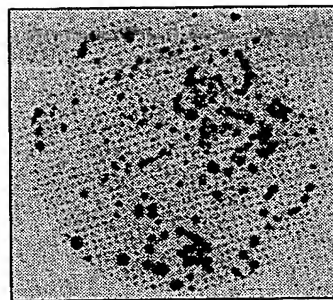


Fig.13.

Q V Q L Q E S G G G L V Q P G G
 CAG GTG CAG CTG CAG GAG TCA GGA GGA GGC TTG GTA CAG CCT GGG GGT
 PstI
 S L R L S C A T S G F T F S N Y
 TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG TTC ACC TTC AGT AAT TAC
 Y M G W V R Q P P G K A L E W L
 TAC ATG GGC TGG GTC CGC CAG CCT CCA GGA AAG GCA CTT GAG TGG TTG
 G S V R N K V N G Y T T E Y S A
 GGT TCT GTT AGA AAC AAA GTT AAT GGT TAC ACA ACA GAG TAC AGT GCA
 S V K G R F T I S R D N F Q S I
 TCT GTG AAG GGG CGG TTC ACC ATC TCC AGA GAT AAT TTC CAA AGC ATC
 L Y L Q I N T L R T E D S A T Y
 CTC TAT CTT CAA ATA AAC ACC CTG AGA ACT GAG GAC AGT GCC ACT TAT
 Y C A R G Y D Y G A W F A Y W G
 TAC TGT GCA AGA GGC TAT GAT TAC GGG GCC TGG TTT GCT TAC TGG GGC
 Q G T L V T v s s g g g g s g g g g s
 CAA GGG ACC CTG GTC ACC gtc tcc tca ggtggaggcgggttcaggcggagggtggctct
 BstEII
 g g g g s d i E L T Q T P L S L P V
 ggcgggtggcggatcgac atc GAG CTC ACC CAA ACT CCA CTC TCC CTG CCT GTC
 SacI
 S L G D Q A S I S C R S S Q S I
 AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT
 V H S N G N T Y L E W Y L Q K P
 GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTG CAG AAA CCA
 PstI
 G Q S P K L L I Y K V S N R F S
 GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT
 G V P D R F S G S G S G T D F T
 GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCG GGG ACA GAT TTC ACA
 L K I S R V E A E D L G V Y Y C
 CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC
 F Q G S H V P Y T F G G G T K L
 TTT CAA GGT TCA CAT GTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTC
 E I K R
GAG ATC AAA CGG (SEQ ID NO. 190)
 XhoI (SEQ ID NO. 191)

Fig.14.

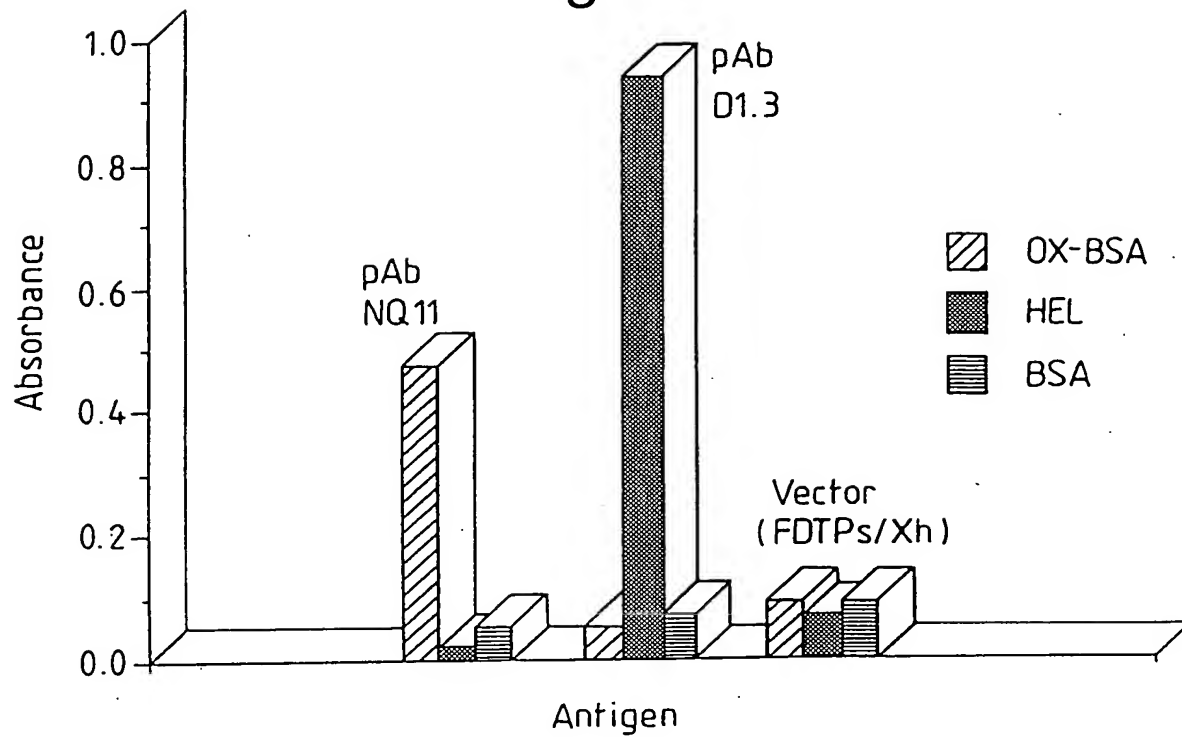


Fig.15.

5' END

TCT CAC AGT GCA CAA ACT GTT GAA CGG ACA CCA GAA ATG CCT GTT CTG (SEQ ID NO:192)
 (SEQ ID NO:193)
 ApaL1

3' END

K A A L G L K (SEQ ID NO:194)
 AAA GCC GCT CTG GGG CTG AAA GCG GCC GCA GAA ACT GTT GAA AGT etc. (SEQ ID NO:195)
 Not I

Fig.16a

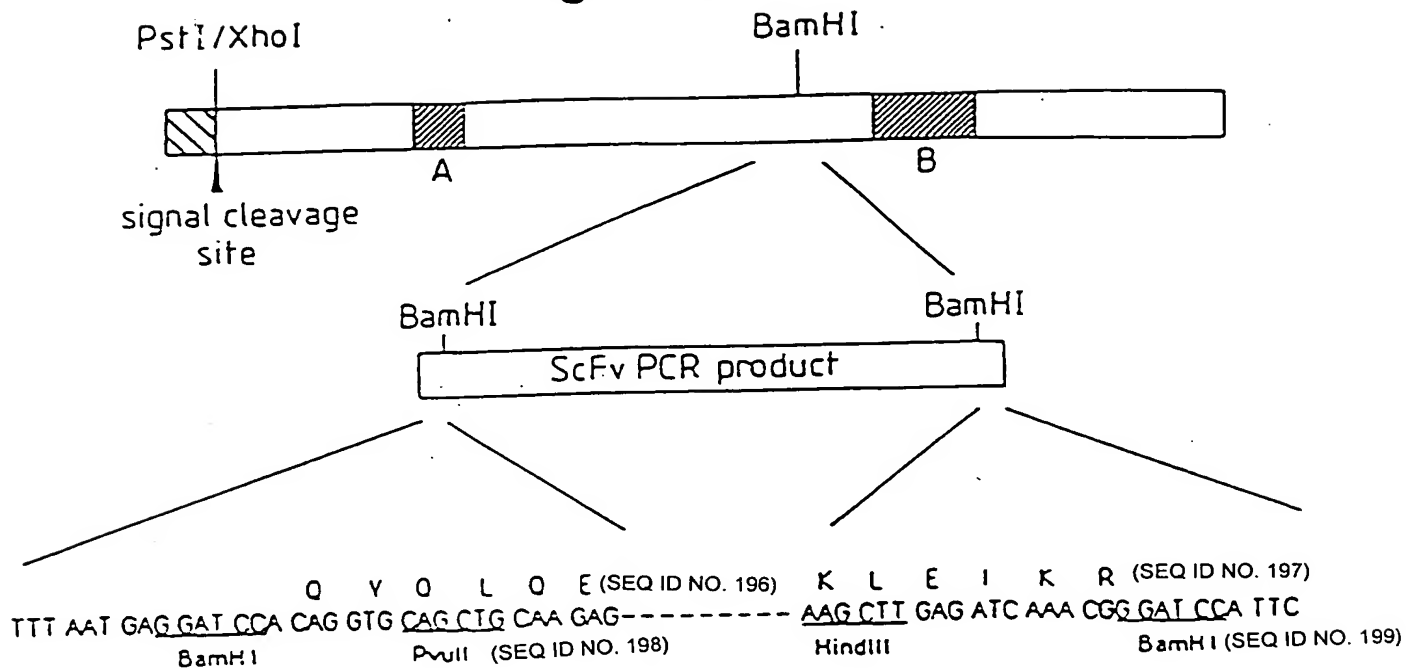
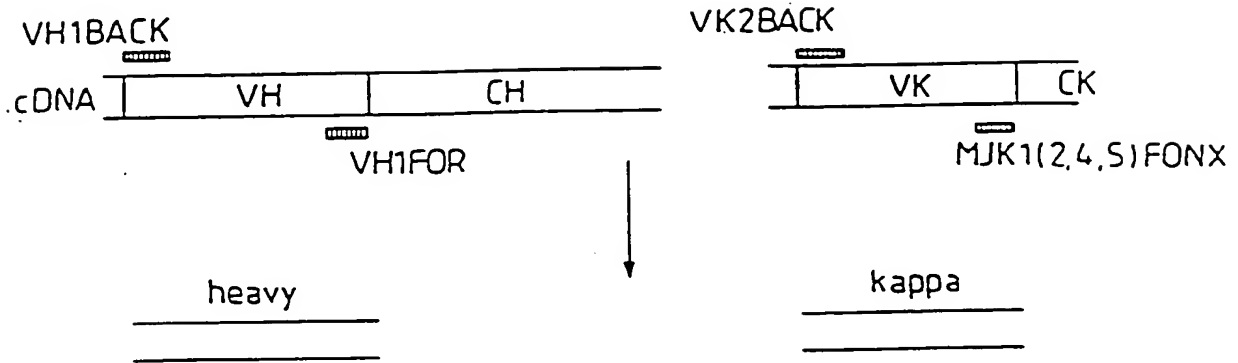


Fig.16b

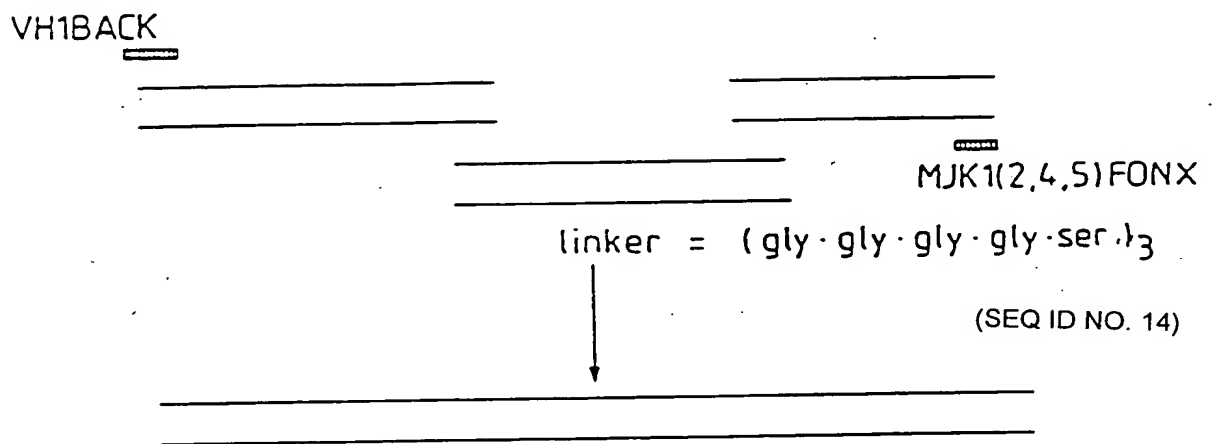
A	(1834)	5'	GAG GGT GGT GGC TCT	(SEQ ID NO. 200)
		-	- -C - -	(SEQ ID NO. 201)
		-	- -C - -	(SEQ ID NO. 202)
		-	- -C - ACT 3'(1839)	(SEQ ID NO. 203)
B	(2284)	5'	GGC GGC GGC TCT	(SEQ ID NO. 204)
		-	GGT GGT GGT -	(SEQ ID NO. 205)
		-	- GGC GGC -	(SEQ ID NO. 206)
		GAG	- - GGC -	(SEQ ID NO. 207)
		-	- - GGT -	(SEQ ID NO. 208)
		-	- - GGC -	(SEQ ID NO. 209)
		-	- - GGT -	(SEQ ID NO. 210)
		-	- - GGC - 3'(2379)	(SEQ ID NO. 211)
Reverse complement of mutagenic oligo G3Bamlink				
		5'	GAG GGT GGC GGA TCC	(SEQ ID NO. 212)
			T	
			GAG GGT GGC GG 3'	(SEQ ID NO. 213)

Fig.17.

1) PRIMARY PCR



2) ASSEMBLY PCR



3) ADDING RESTRICTION SITES

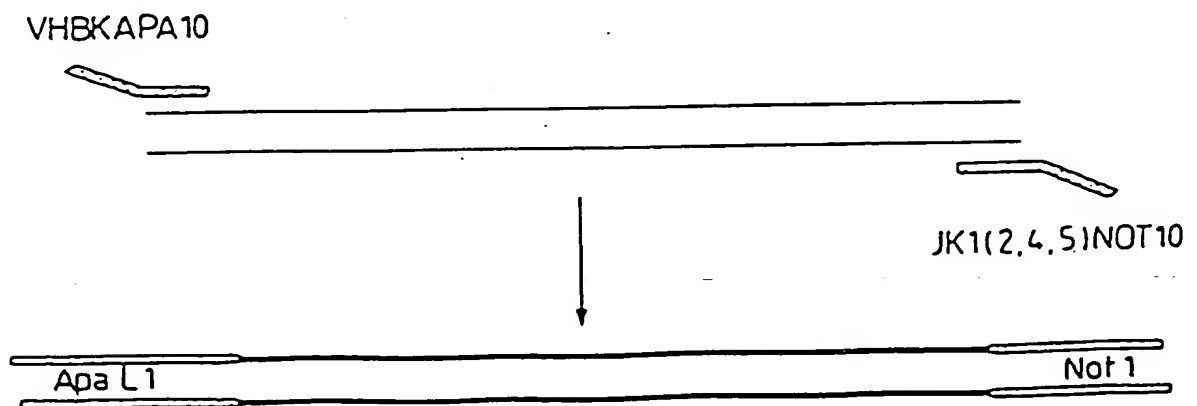


Fig.18.

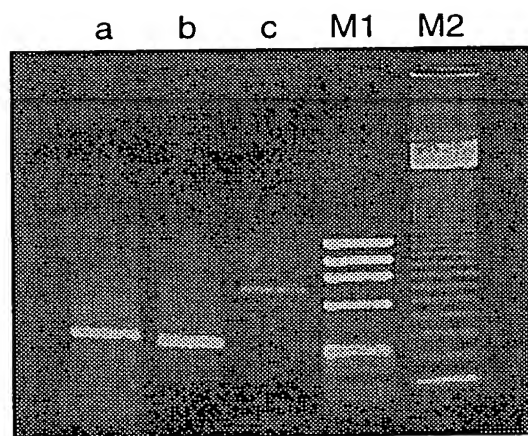


Fig.19.

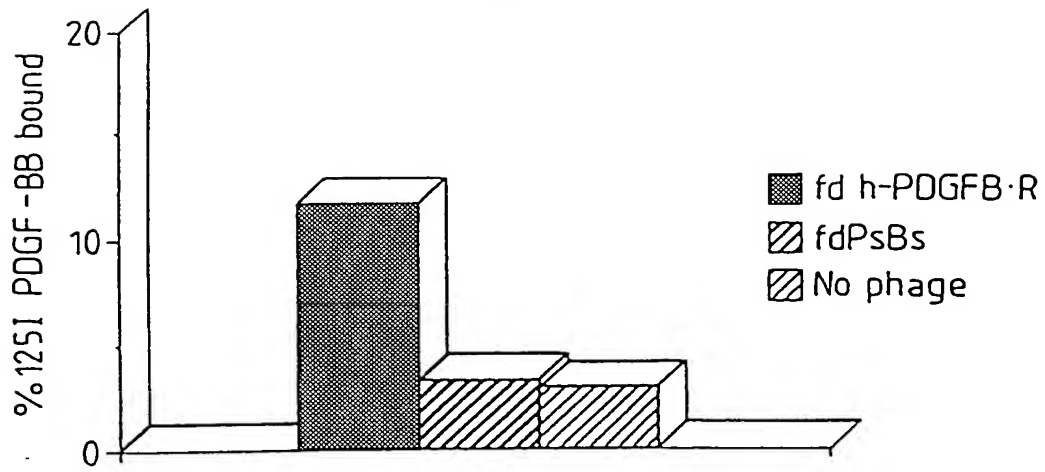


Fig.20.

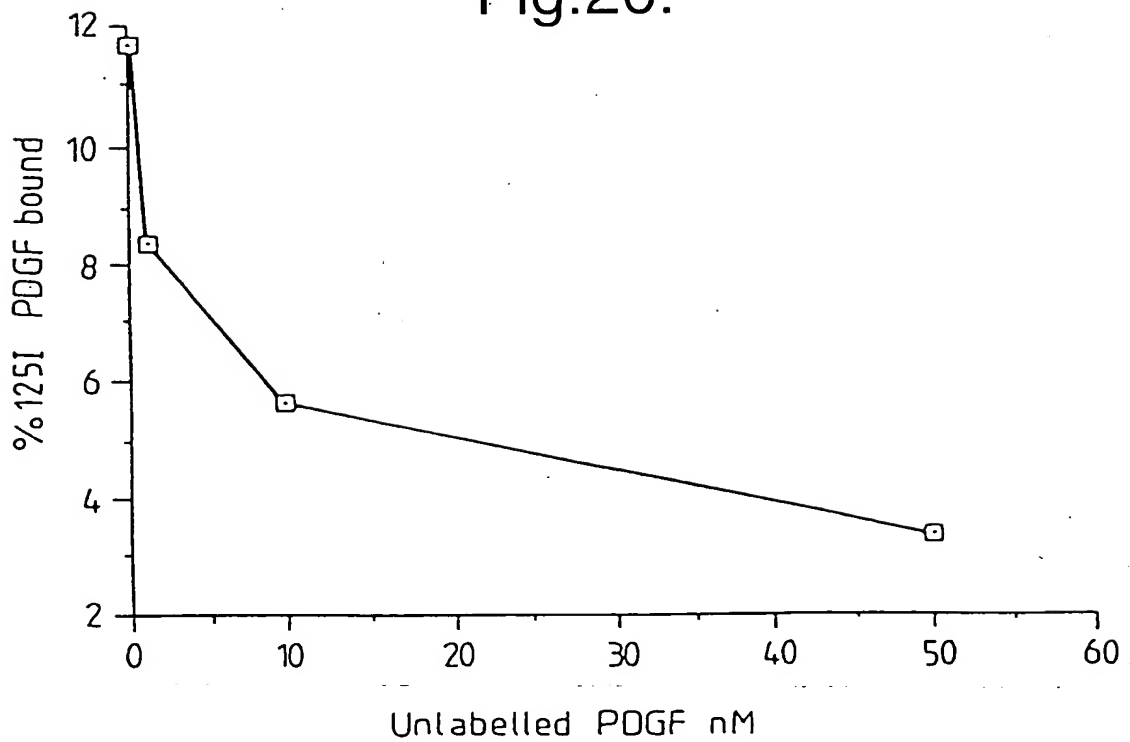


Fig.21.

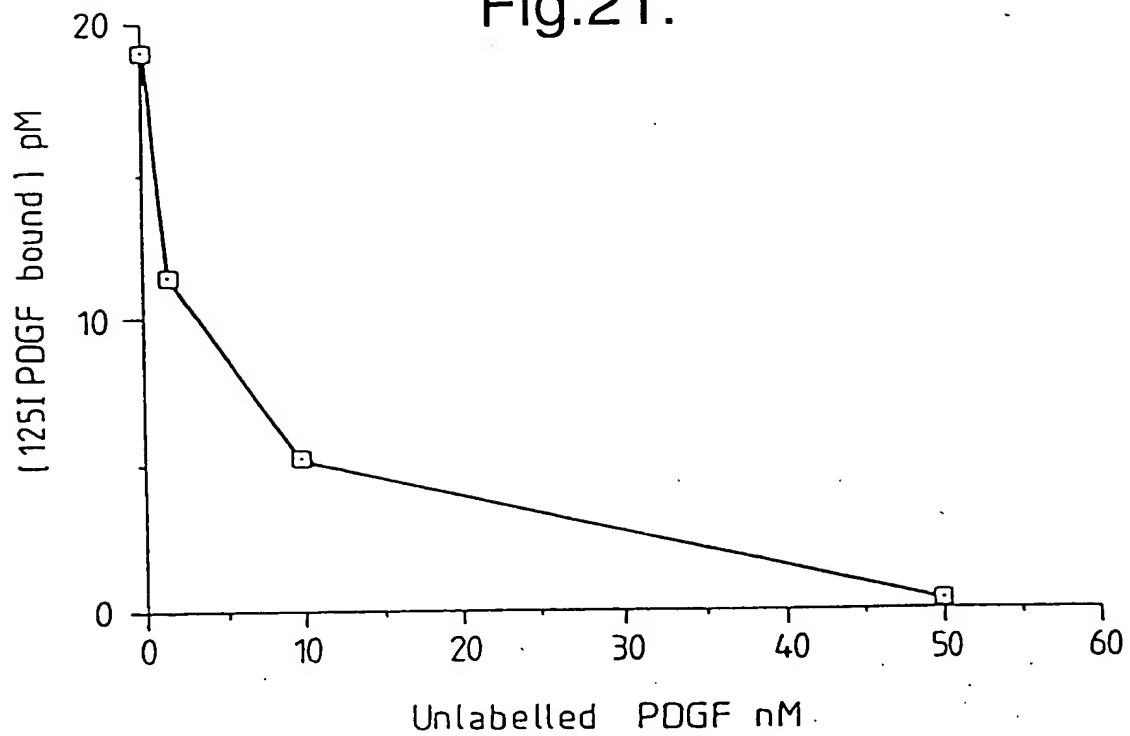


Fig.22.

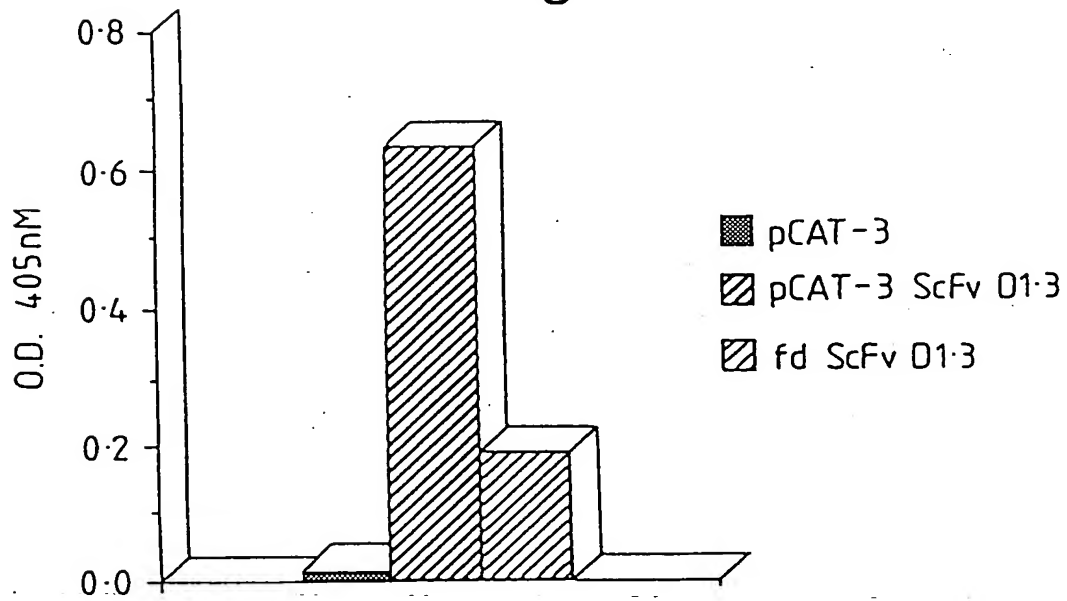


Fig.23a

d
M

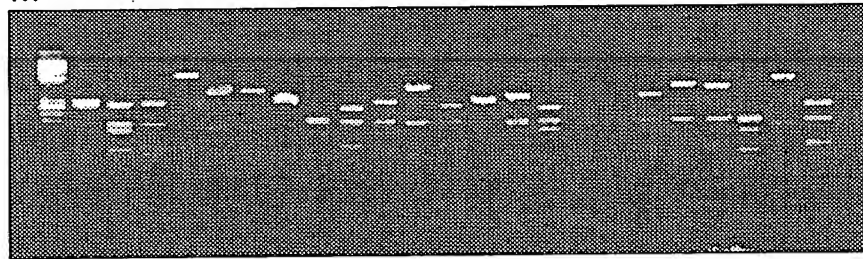
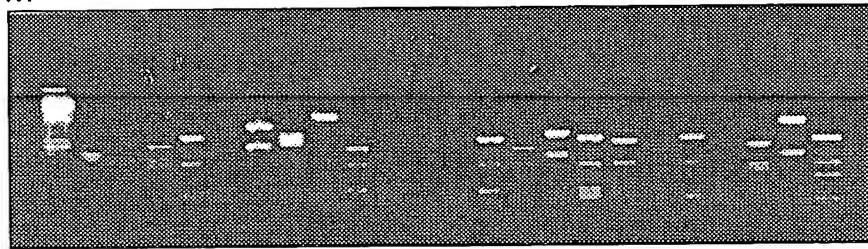


Fig.23b

M



VH sequences

Fig.24a

from combinatorial library:

	CDR1	CDR2	CDR3		(SEQ ID NO. 214)
A	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x4	(SEQ ID NO. 215)
B	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x9	(SEQ ID NO. 216)
C	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 217)
D	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 218)
E	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 219)
F	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 220)
G	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 221)
H	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 222)

from hierarchical library VH-rep x V κ -d:

	CDR1	CDR2	CDR3		(SEQ ID NO. 223)
I	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 224)
J	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 225)
K	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 226)
L	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 227)
M	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 228)
N	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 229)
O	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 230)
P	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 231)
Q	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 232)
R	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 233)
S	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 234)
T	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 235)
U	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 236)
V	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 237)
W	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 238)
X	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 239)
Y	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 240)
Z	QVQLQSGSGLASGATGASVTHSSCKASGTTT	YINPSEGTYTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 241)

Fig.24b

V κ sequences

from combinatorial library:

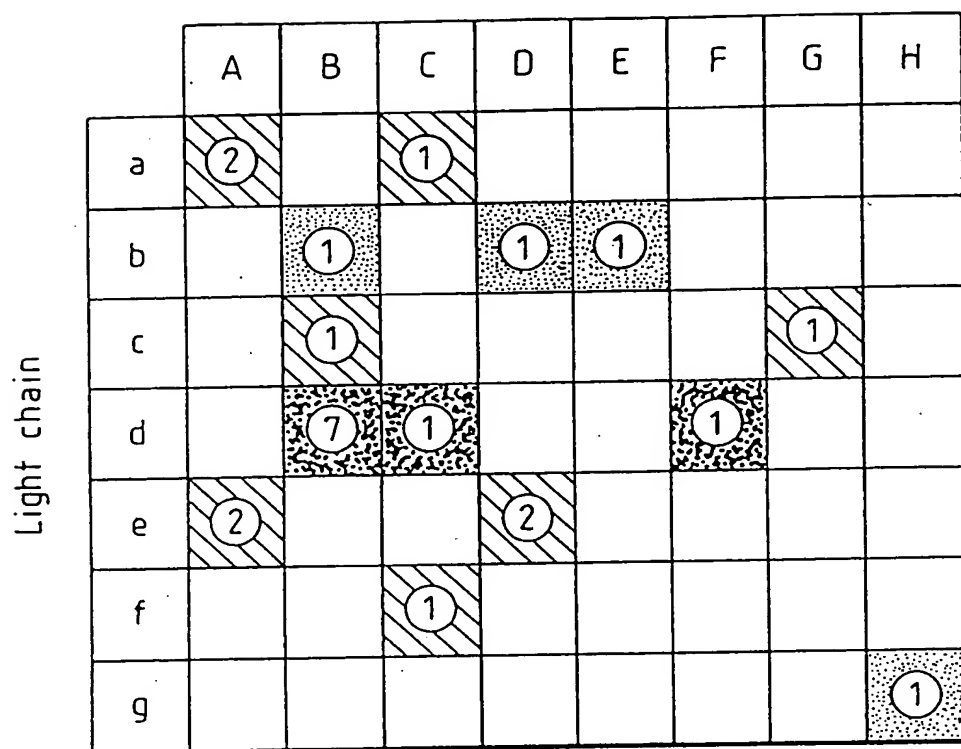
	CDRI	CDR2	CDR3		
a	DIELTQSPSSLSASLGERVSLTC	WLOQKPDGSIKRLIY	LOYASYPT	FGACTKLEIKRA X3	V (SEQ ID NO. 236)
b	DIELTQSPA IHSASPGCKVTHTC	MYQOKSGASPKRMII	QOYSGYPLT	FGACTKLEIKRA X3	IV (SEQ ID NO. 237)
c	DIELTQSPPTTHAASPGCKITITC	MYQOKPGFSPKLLIY	QOGSSIPLT	FGACTKLEIKRA X3	IV (SEQ ID NO. 238)
d	DIELTQSPPTTHAASPGCKITITC	MYQOKPGFSPKLLIS	QOGSTIPFT	FGSTKLEIKRA X9	IV (SEQ ID NO. 239)
e	DIELTQSPA IHSASPGCKVTHTC	MYQOKPCTSPKLMII	QQRSSYPPT	FGSTKLEIKRA X4	VI (SEQ ID NO. 240)
f	DIELTQSPA IHSASPGCKVTHTC	MYQOKSGTSPKRMII	QOFSNIPLT	FGACTKLEIKRA	VI (SEQ ID NO. 241)
g	DIELTQSPA IHSASPGCKVTHTC	MYQOKPGASPKRMII	IQRNSYPHT	FGCTKLEIKRA	VI (SEQ ID NO. 242)

from hierarchical library VH-B x V κ -rep:

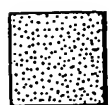
h	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	DTSKLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QQMSNPIT	FGACTKLEIKRA X4	IV/VI	V κ ox1	(SEQ ID NO. 243)
i	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	STSNLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGACTKLEIKRA	V	ox-1ike?	(SEQ ID NO. 244)
j	DIELTQSPPTTHAASPGCKITITC	SASSSVSTRI	RTSNLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOGSSIPLT	FGCTKLEIKRA	V	ox-1ike	(SEQ ID NO. 245)
k	DIELTQSPPTTHAASPGCKITITC	SATS6ISSNYLH	RTSNLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOGSSIPYT	FGCTKLEIKRA	V	ox-1ike	(SEQ ID NO. 246)
l	DIELTQSPPTTHAASPGCKITITC	SASSSVSTRI	RTSNLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOGSSIPYT	FGCTKLEIKRA	V	ox-1ike	(SEQ ID NO. 247)
m	DIELTQSPPTTHAASPGCKITITC	SASSSVSTRI	RTSNLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOGSSIPYT	FGCTKLEIKRA	V	ox-1ike	(SEQ ID NO. 248)
n	DIELTQSPPTTHAASPGCKITITC	SASSSVSTRI	RTSNLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOGSSIPYT	FGCTKLEIKRA	V	ox-1ike	(SEQ ID NO. 249)
o	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	RTSNLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOGSSIPYT	FGCTKLEIKRA X3	V	ox-1ike	(SEQ ID NO. 250)
p	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	DTSKLAS	CVPARFSGSGSCTSYSLTIGTHEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA X3	IV/VI	V κ ox1	(SEQ ID NO. 251)
q	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	DTSKLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	V κ ox1	(SEQ ID NO. 252)
r	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	DTSKLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	V κ ox1	(SEQ ID NO. 253)
s	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	STSNLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	ox-1ike	(SEQ ID NO. 254)
t	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	STSNLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	ox-1ike	(SEQ ID NO. 255)
u	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	STSNLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	ox-1ike	(SEQ ID NO. 256)
v	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	STSNLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	ox-1ike	(SEQ ID NO. 257)
w	DIELTQSPA IHSASPGCKVTHTC	SASSSVSTRI	STSNLAS	CVPARFSGSGSCTSYSLTISSEAEADAATTC	QOYHSYPLT	FGCTKLEIKRA	IV/VI	ox-1ike	(SEQ ID NO. 258)

Fig.25.

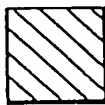
HEAVY CHAIN



OD_{405nm} in ELISA



0.2-0.9



0.9-2.0



>2.0

Fig.26(a).

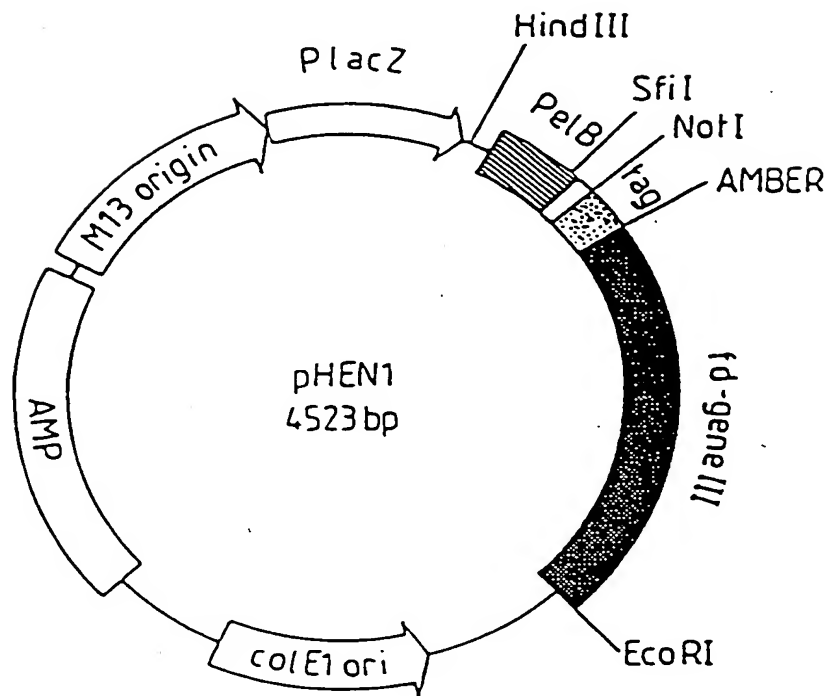


Fig.26(b).

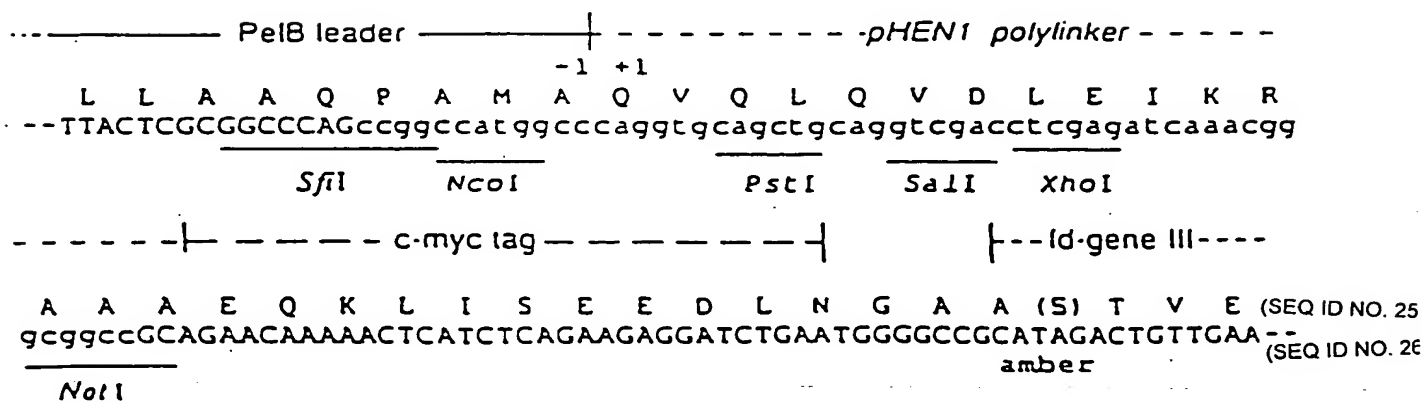


Fig.27.

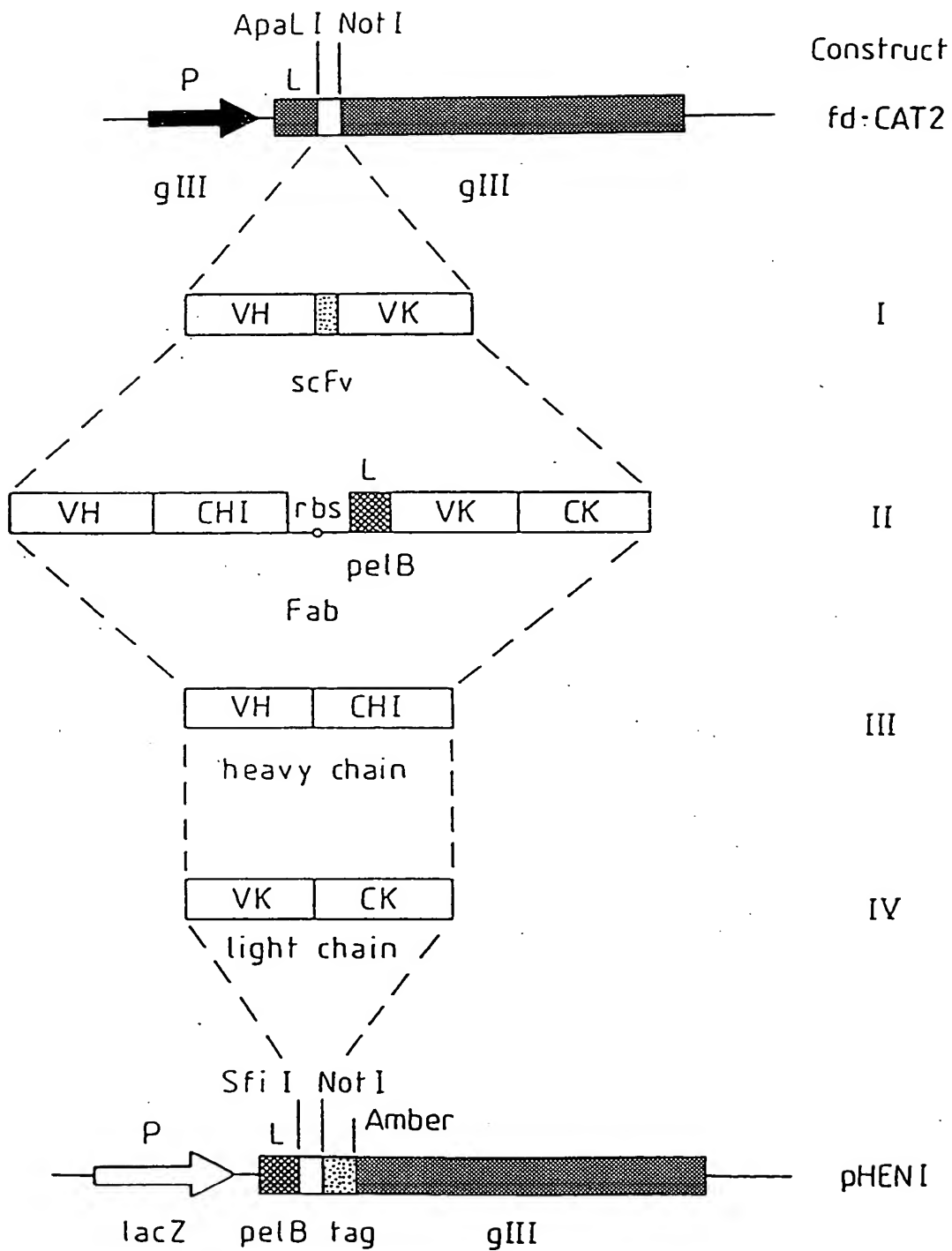


Fig.28.

Fab

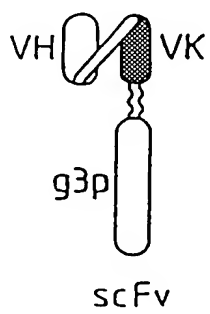
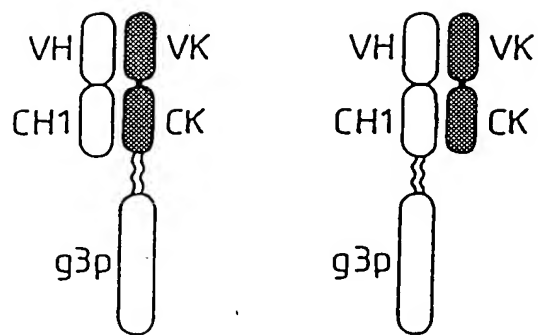


Fig.29.

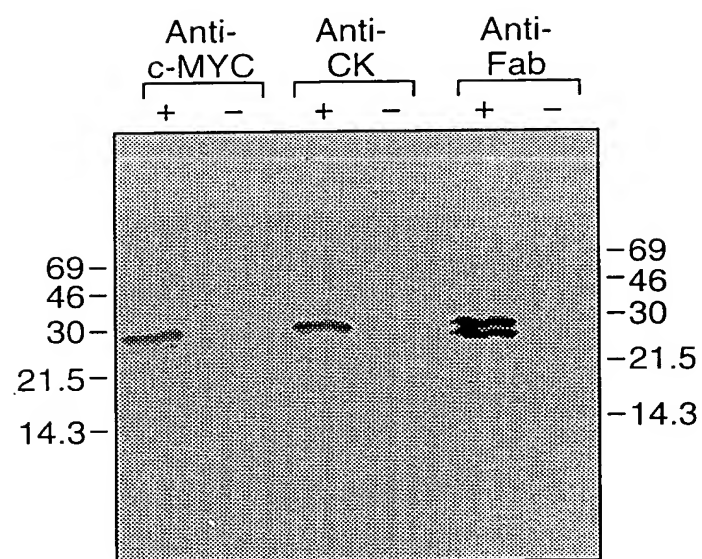


Fig.30.

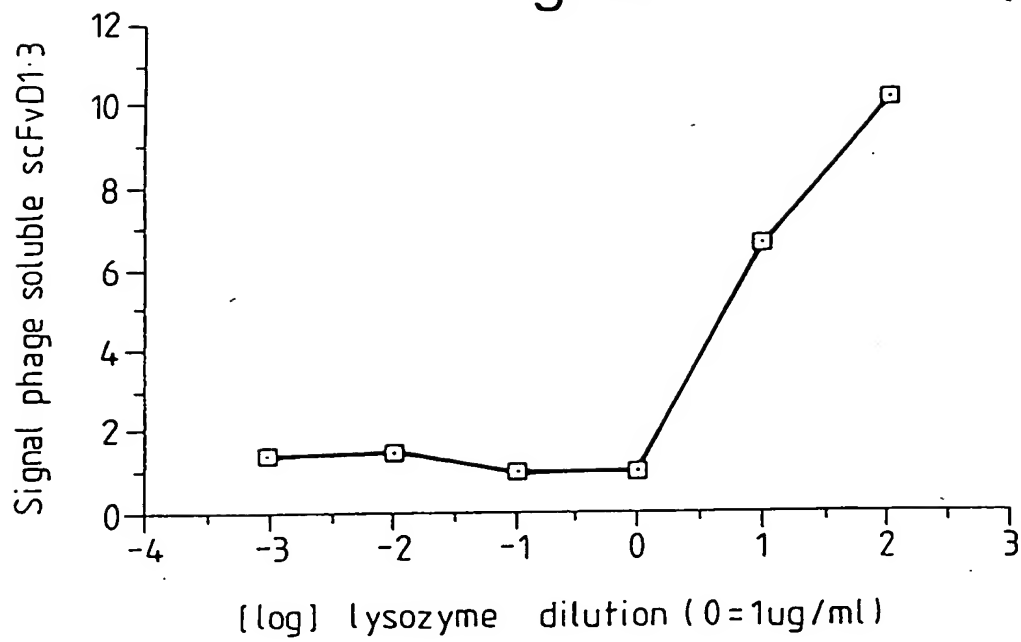


Fig.31.

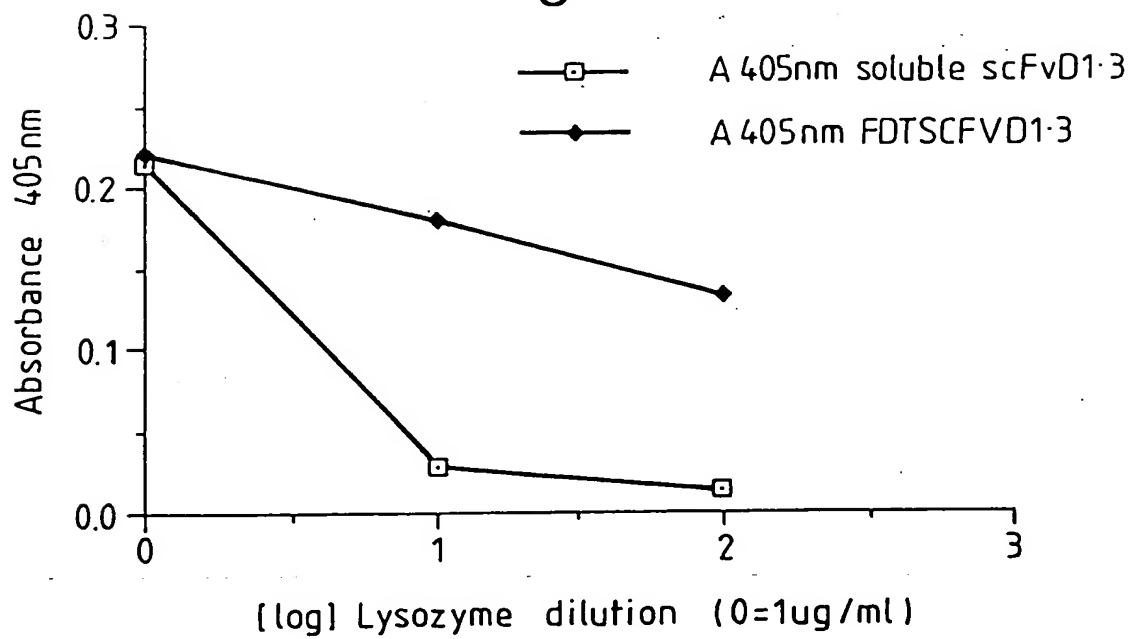


Fig.32.

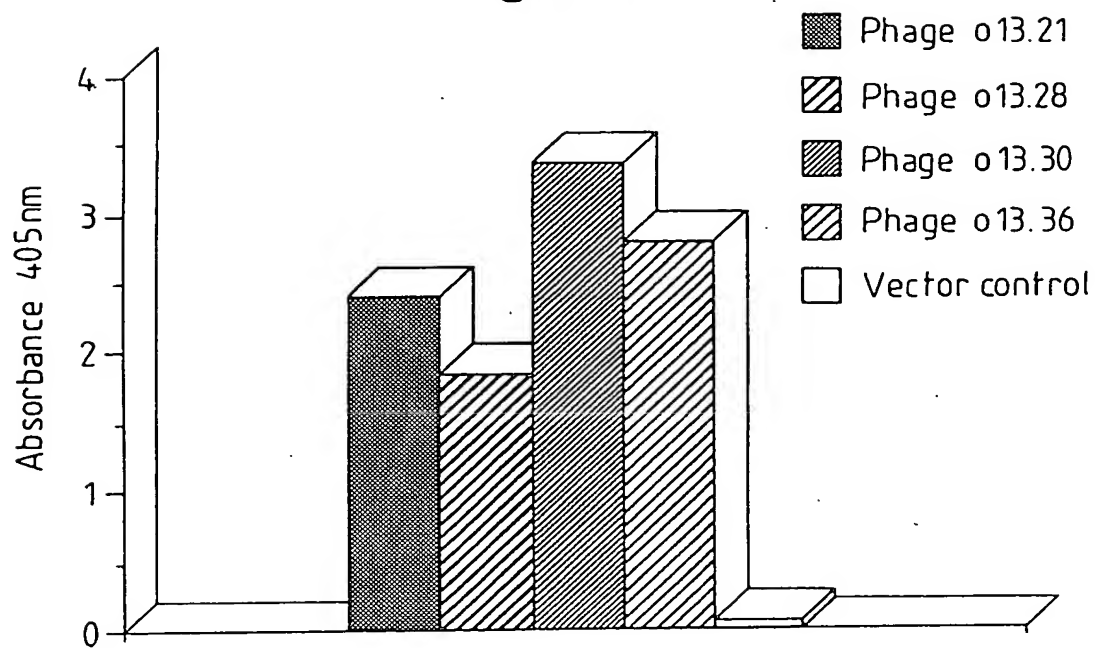


Fig.33.

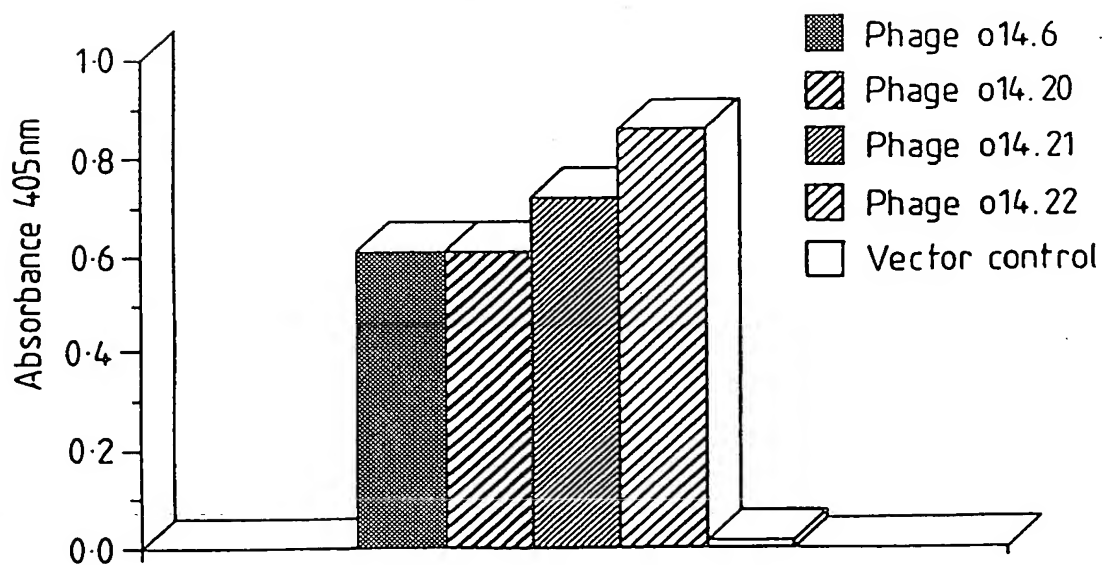


Fig.34.

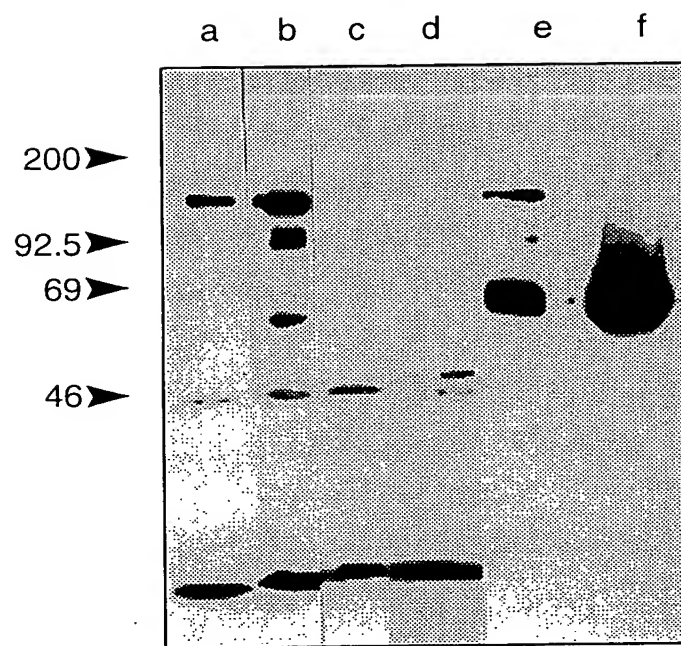


Fig.35A.

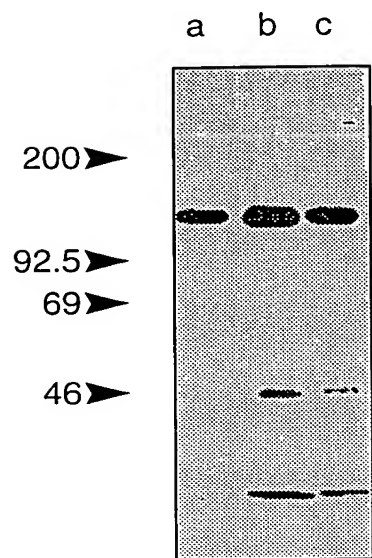


Fig.35B.

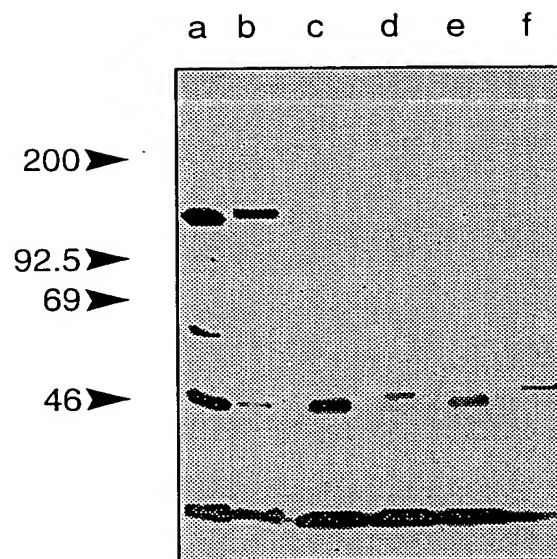


Fig.36.

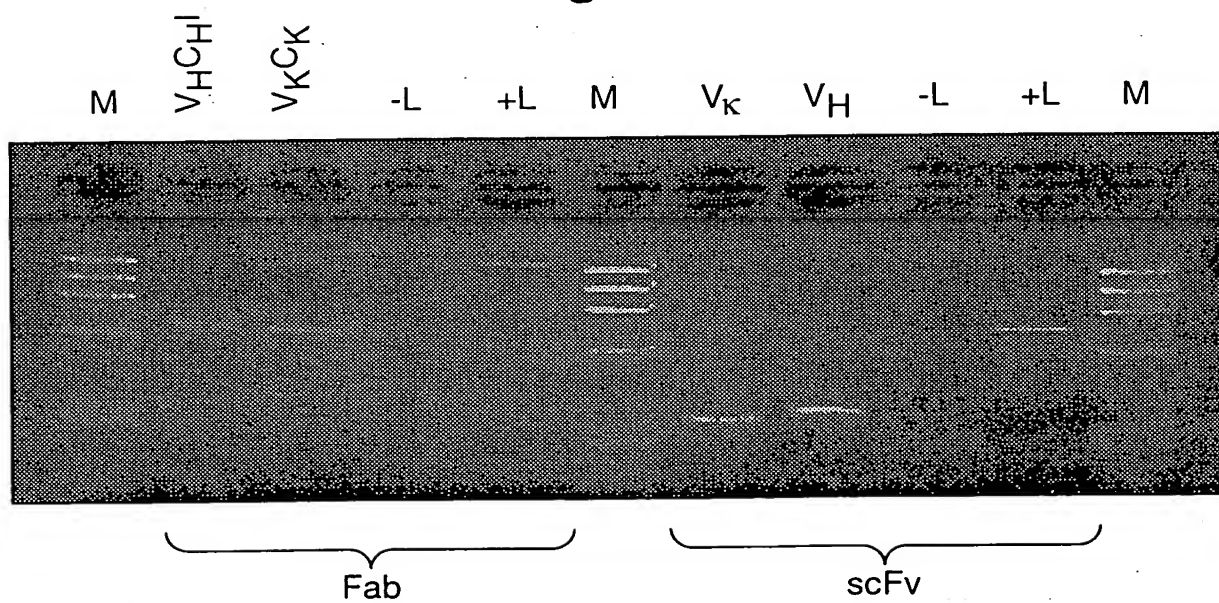


Fig.37.

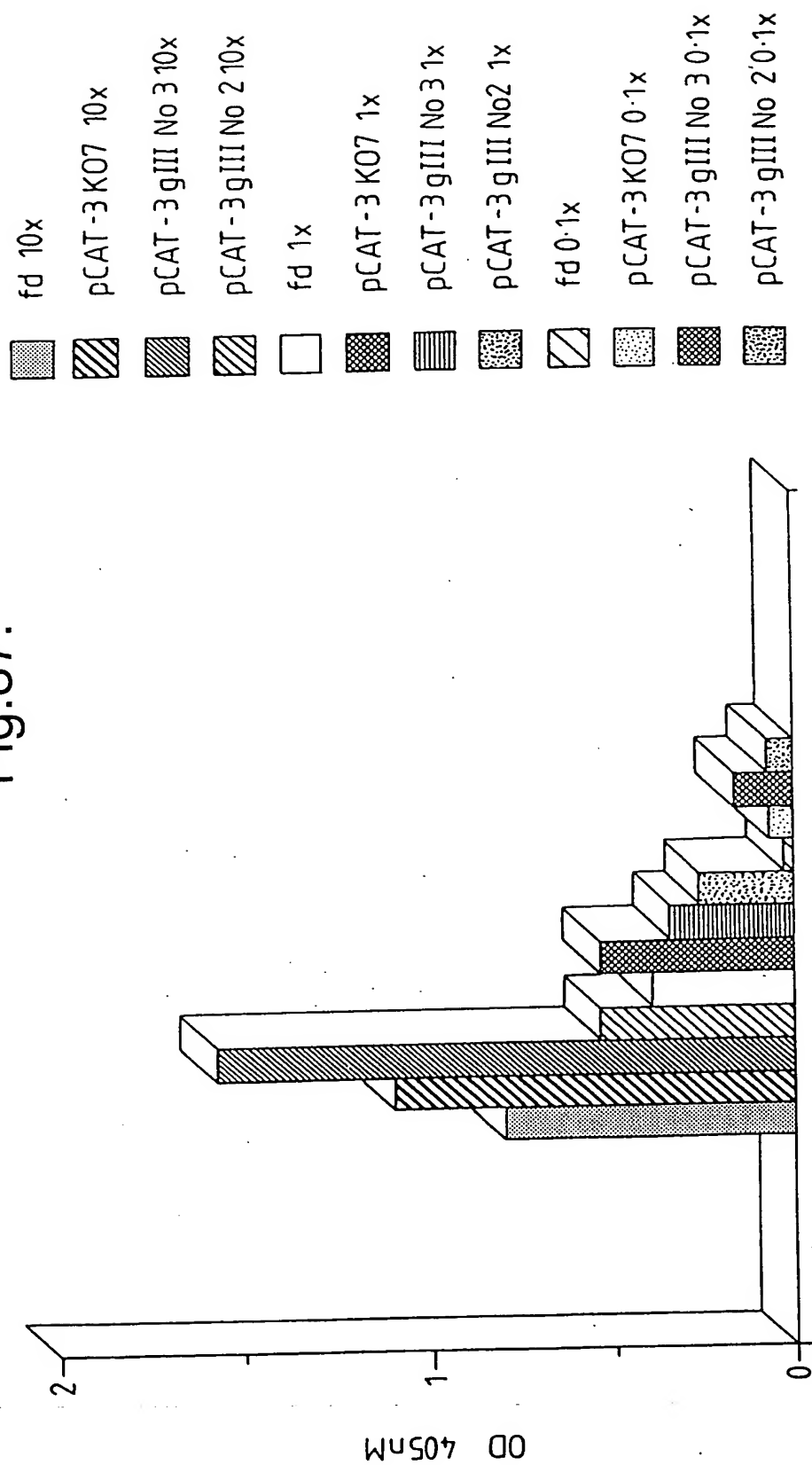


Fig.38A.

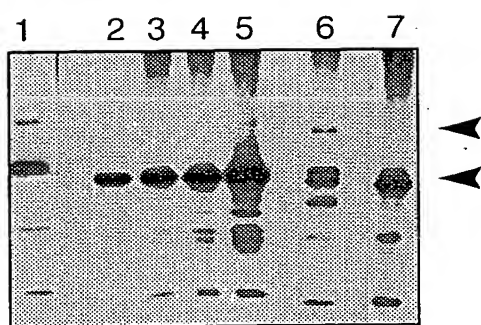


Fig.38B.

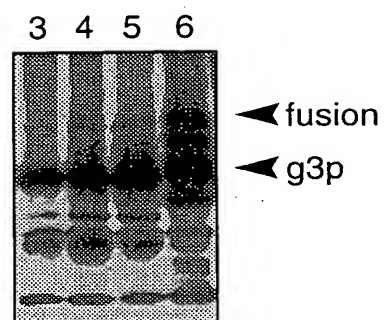


Fig.39.

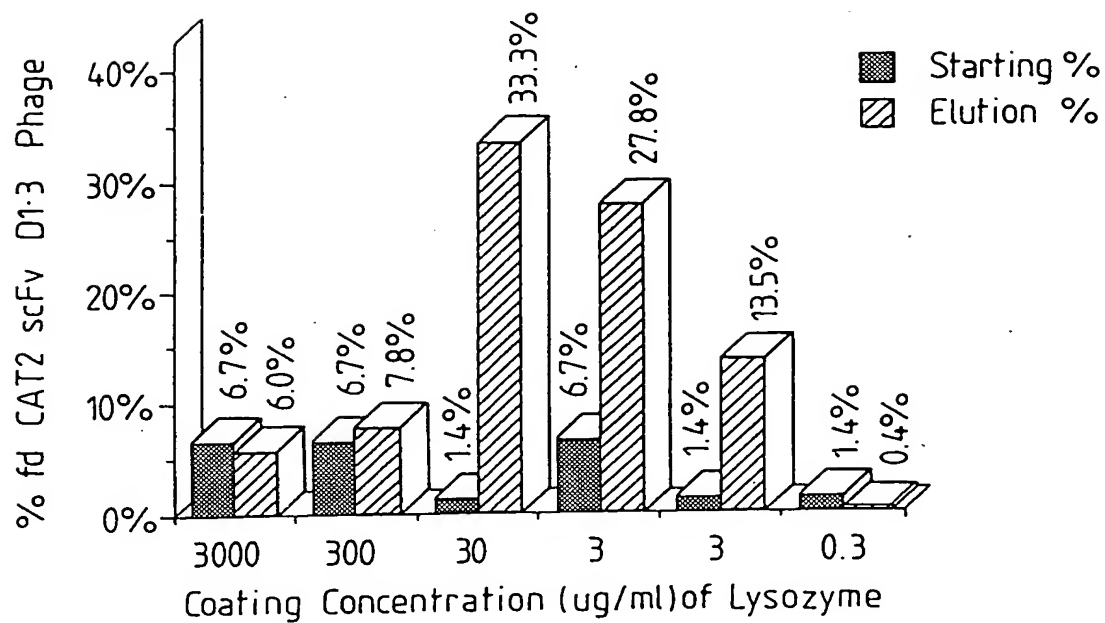


Fig.40.

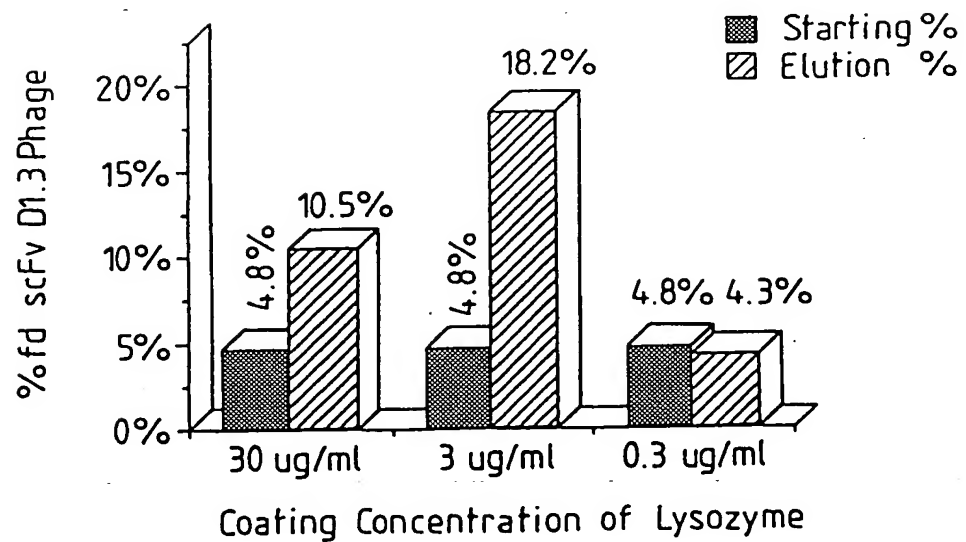


Fig.41.

1 2

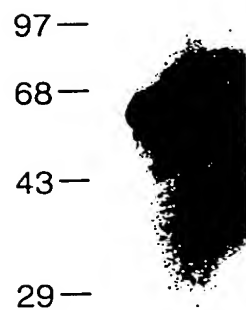


Fig.42.

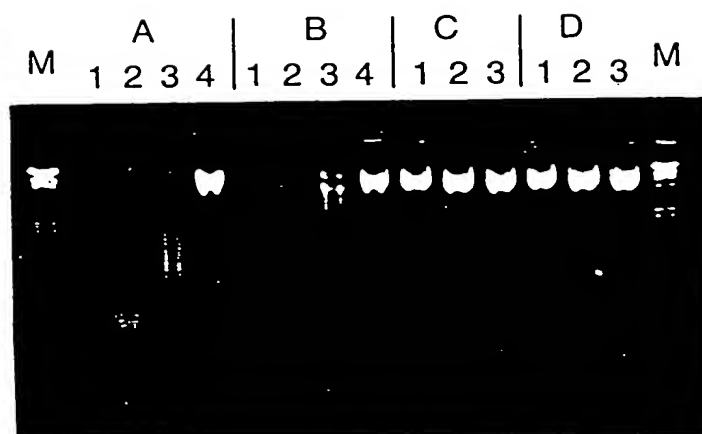


Fig.43.

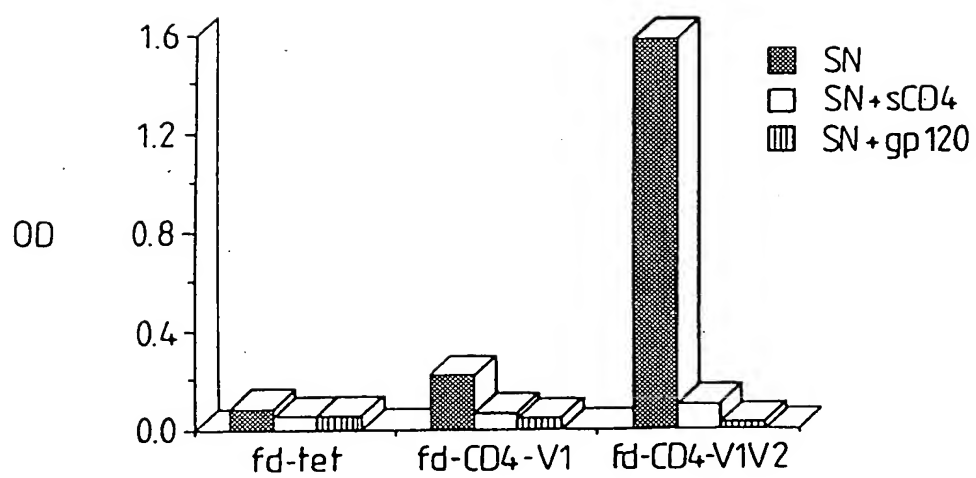


Fig.44a

10	20	30	40	50	60	70	80	90
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTGTCTCCTGCAAGGCT								
AAGATAAGAGTGTACCGTGTCCAGGTCGACGTCGTCAGACCCCGACTCGAACACTTCGGACCCCGAAGTCACTTCGACAGGACGTTCCGA								
PheTyrSerHisSerAlaGlnValGlnLeuGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAla								
100	110	120	130	140	150	160	170	180
TCTGGCTACACCTTCACCAGCTACTGGATGCACCTGGGTGAAGCAGAGGCCCTGGACGAGCCCTTGAGTGGATTGGAAGGATTGATCCTAAT								
AGACCGATGTGGAAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGGACCTGCTCCGGAACCTCACCTAACCTTCCTAACTAGGATTA								
SerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgProGlyArgGlyLeuGluTrpIleGlyArgIleAspProAsn								
190	200	210	220	230	240	250	260	270
AGTGGTGGTACTAAGTACAAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCCTCCAGCACAGCCTACATGCAGCTCAGC								
TCACCACCATGATTTCATGTTACTCTTCAAGTTCTCGTTCGGGTGTGACTGACATCTGTTTGGAGGTCGTGTGGATGTACGTCGAGTCG								
SerGlyGlyThrLysTyrAsnGluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSer								
280	290	300	310	320	330	340	350	360
AGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTACTACTTTGACTACTGGGCCAAGGGACC								
TCGGACTGTAGACTCCTGAGACGCCAGATAATAACACGTTCTATGCTGATGCCATCATCGATGATGAAACTGATGACCCCGGTTCCCTGG								
SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrAspTyrGlySerSerTyrTyrPheAspTyrTrpGlyGlnGlyThr								
370	380	390	400	410	420	430	440	450
ACGGTCACCGTCTCCTCNGGTGGAGCGGTTCAAGCGGAGGTGGCTCTGGCGGTGGCGGATCCAGGCTGTTGGGACACAGGAATCTGCA								
TGCCAGTGGCAGAGGAGTCCACCTCCGCCCAAGTCCGCCCTCCACCGAGACCGCCACCGCTAGGGTCCGACACACCCCTGTGTCCTTAGACGT								
ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlnAlaValGlyThrGlnGluSerAla								
460	470	480	490	500	510	520	530	540
CTCACACATCACCTGGTGAACAGTCACACTCACTTGTTCGCTCAAGTACTGGGGCTGTATCAACTAGTAACCTATGCCAACTGGGTCCAA								
GAGTGGTGTAGTGACCACTTTGTGTCAGTGTGAGTGAAACAGCGAGTTTCATGACCCCGACAATGTTGATCATTTGATACGTTGACCCAGGTT								
LeuThrThrSerProGlyGluThrValThrLeuThrCysArgSerSerThrGlyAlaValThrThrSerAsnTyrAlaAsnTrpValGln								
550	560	570	580	590	600	610	620	630
GAAAACACGATCATTTATTCACTGGTCTAATAGGTGTACCAACAACCGAGCTCCAGGTGTTCTCTGCCAGATTCTCAGGCTCCCTTGATT								
CTTTTGGTCTAGTAAATAAGTGACCAGATTATCCACCATGGTTGTTGGCTCGAGGTCCACAGGACGGTCTAAGAGTCCGAGGACTAA								
GluLysProAspHisLeuPheThrGlyLeuIleGlyGlyThrAsnAsnAlaProGlyValProAlaArgPheSerGlySerLeuIle								

Fig.44 b

640	650	660	670	680	690	700	C	G	710	720
GGAGACAAGGCTGCCCCCTCACCATCACAGGGGCACAGACTGAGGATGAGGCANTATATTCTGTGCTCTATGGTACAGCAACCAATTGGGTG										
CCTCTGTTCCGACGGAGTGGTAGTGTCCTCCCGTGTCTGACTCCTACTCCGTTATATAAGACACGAGATACCATGTGCTGGTAACCCAC										
GlyAspLysAlaAlaLeuThrIleThrGlyAlaGlnThrGluAspGluAlaIleTyrPheCysAlaLeuTrpTyrnberAsnHisTrpVal										
730	740	750	760	770						
TTCGGTGAGGAAACCAAACTGACTGTCTCGAGATCAAAACGGCGGCCGC										
AAGCCACCTCCTTGCTTGACTGACAGGAGCTCTAGTTGCCCGCCGCGG										
PheGlyGlyGlyThrLysLeuThrValLeuGluIleLysArgAlaAla										

(SEQ ID NO. 261)

(SEQ ID NO. 262)

Fig.45.

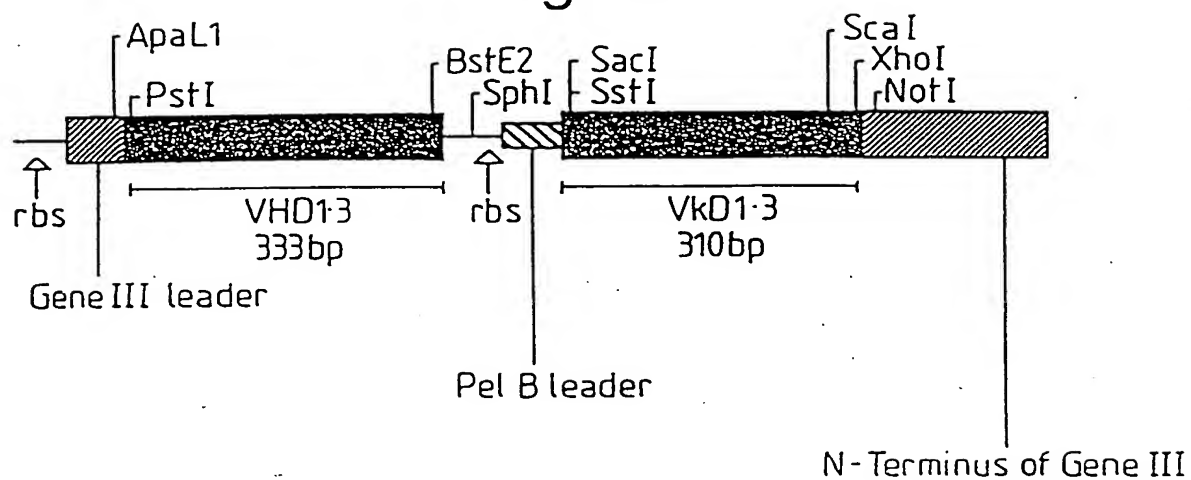


Fig.46.

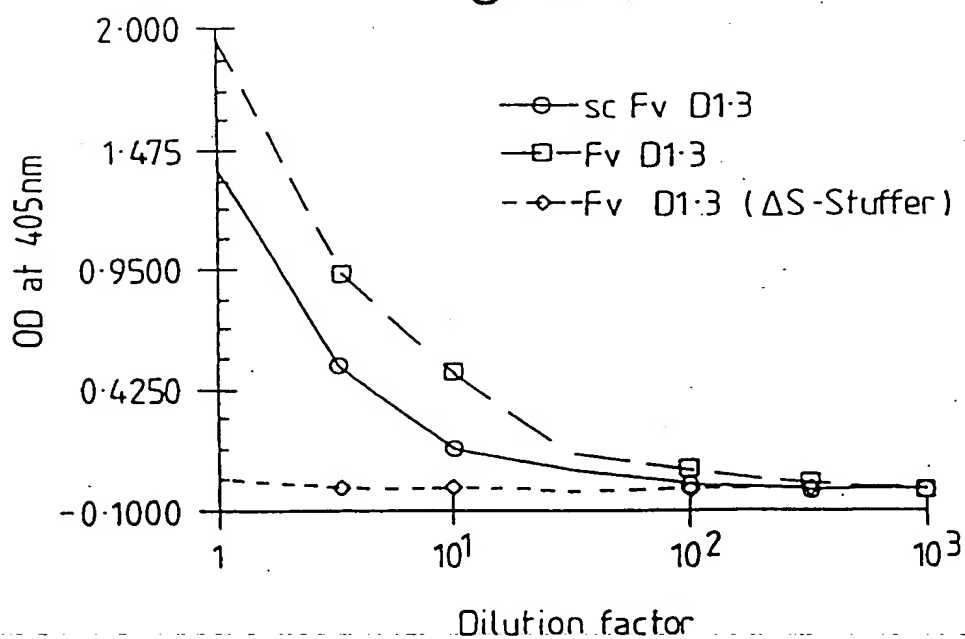


Fig.47.

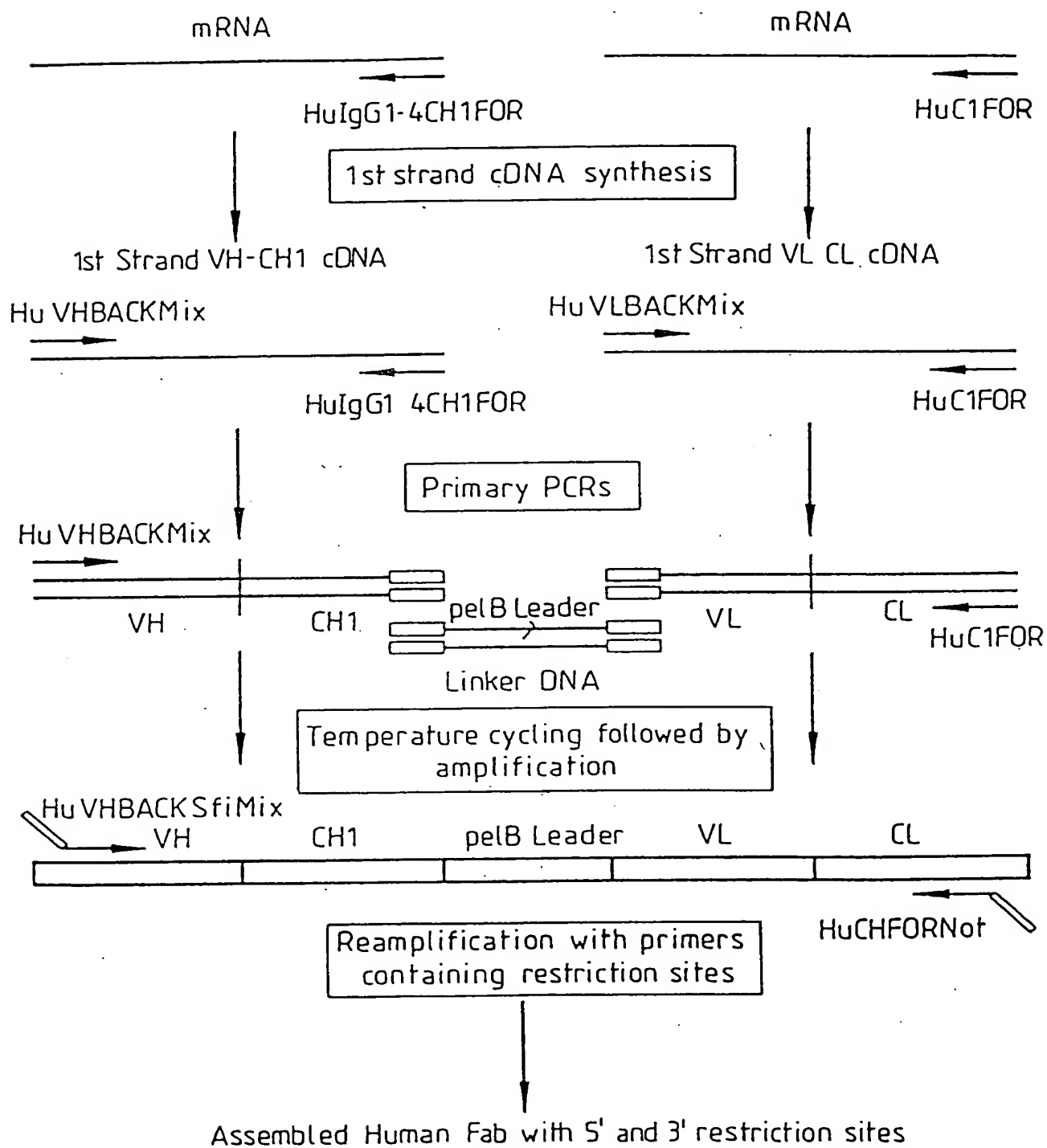


Fig. 48a

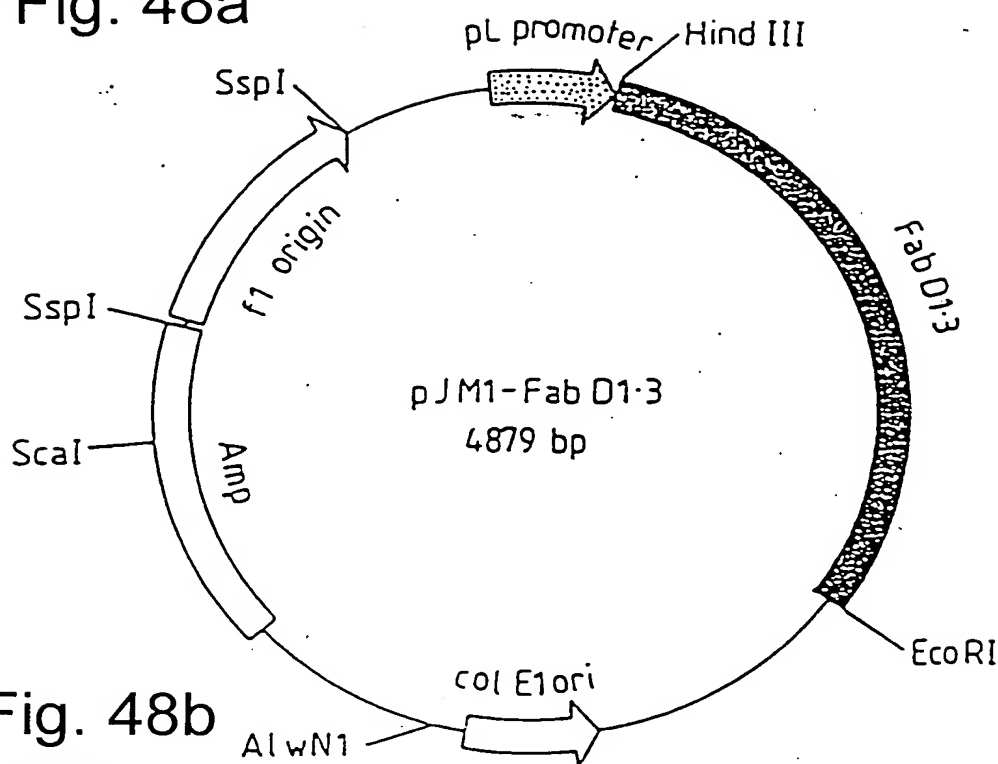


Fig. 48b

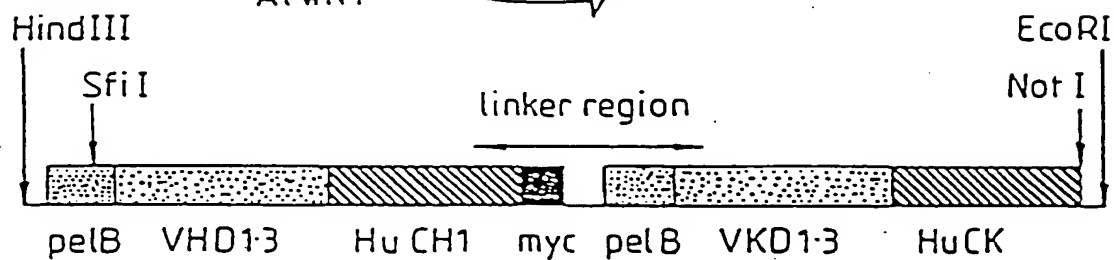


Fig. 48c

← 3' Human CH1 and hinge →
 K P S N T K V D K K V E P K S S T K T H T
 AACCCAGCAACACCAAGGTCGACAAGAAAGTTGAGCCAAATCTTCAACTAAGACGCACACA

→ myc peptide tag →
 S G G E Q K L I S E E D L N * *
 TCAGGAGGTGAACAGAAGCTCATCTCAGAGAGGATCTGAATTATAAGGGAGCTTGCATGCA

(SEQ ID NO. 263)

← pelB leader →
 M K Y L L P T A A A G L
 AATTCTATTTCAGGAGACAGTCATAATGAATAOCTATTGCCTACGGCAGCCGCTGGATTGT

→ 5' Vk →
 L L P A A Q P A M A D I E L T Q S P
 TATTACCTGCTGCCCAACCAGGATGGGCGACATCGAGTTACCCAGTCTCC

(SEQ ID NO. 264)
 (SEQ ID NO. 265)

Fig.49.

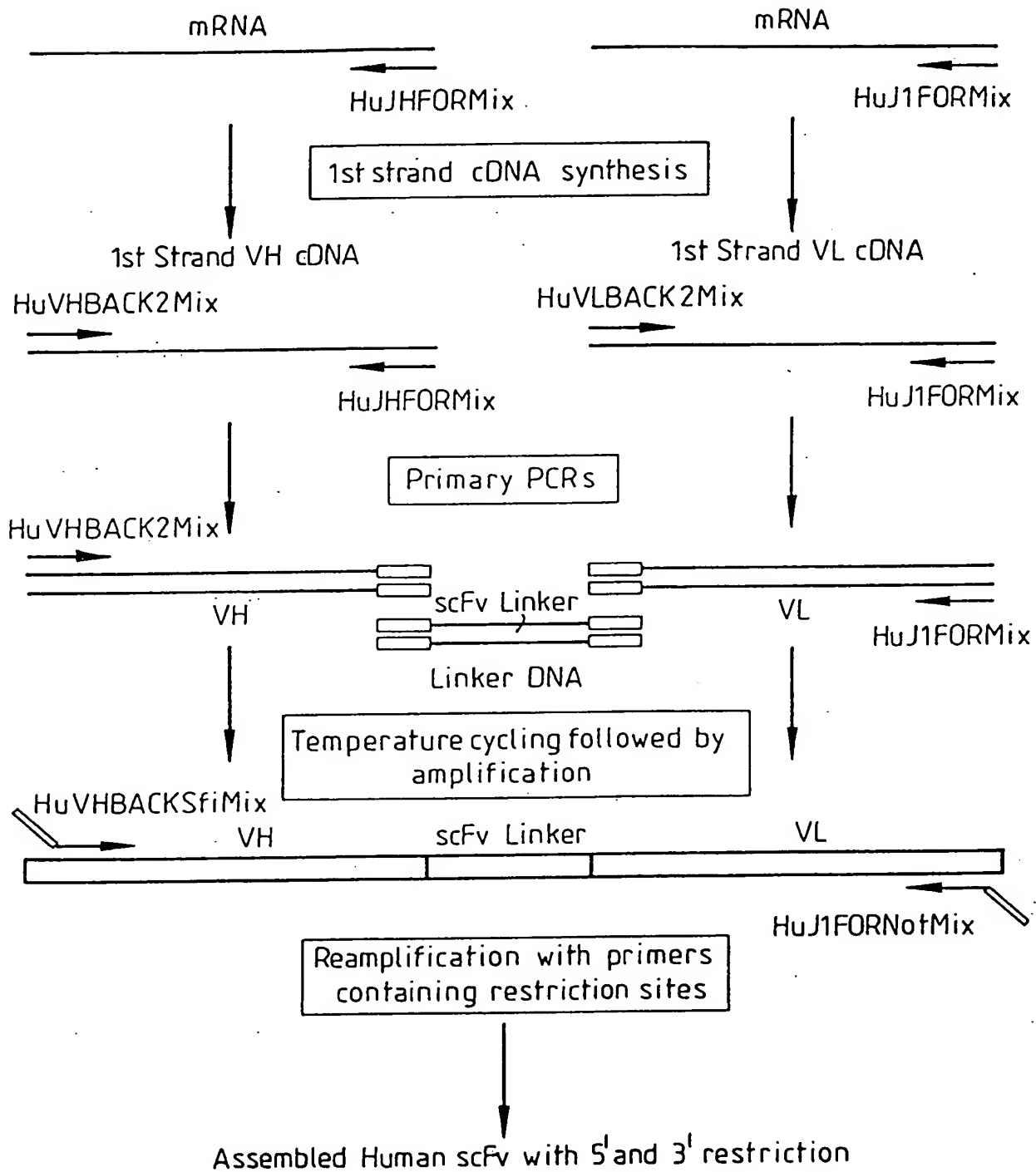


Fig.50a

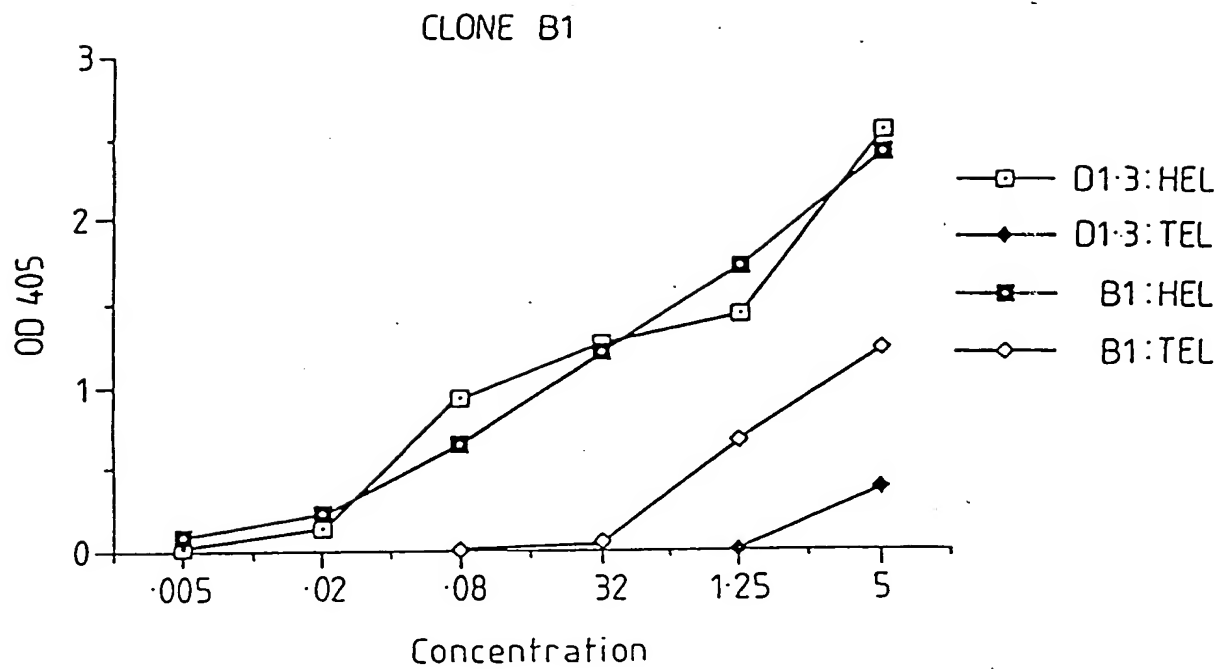


Fig.50b

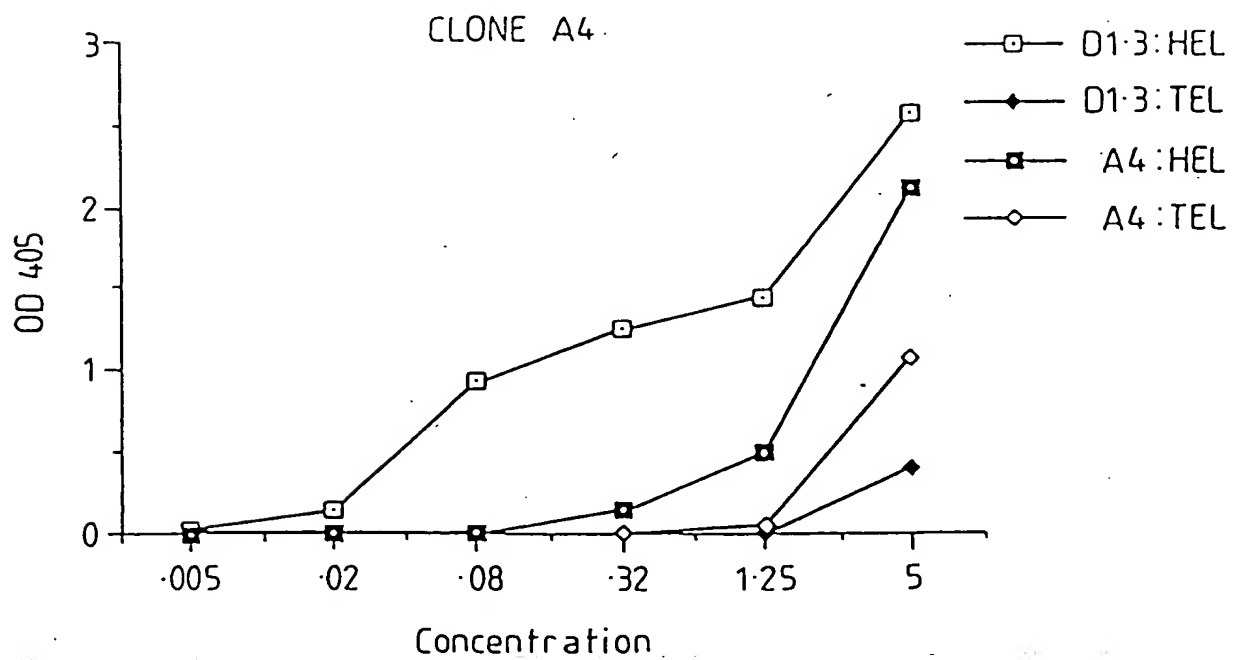


Fig.51.

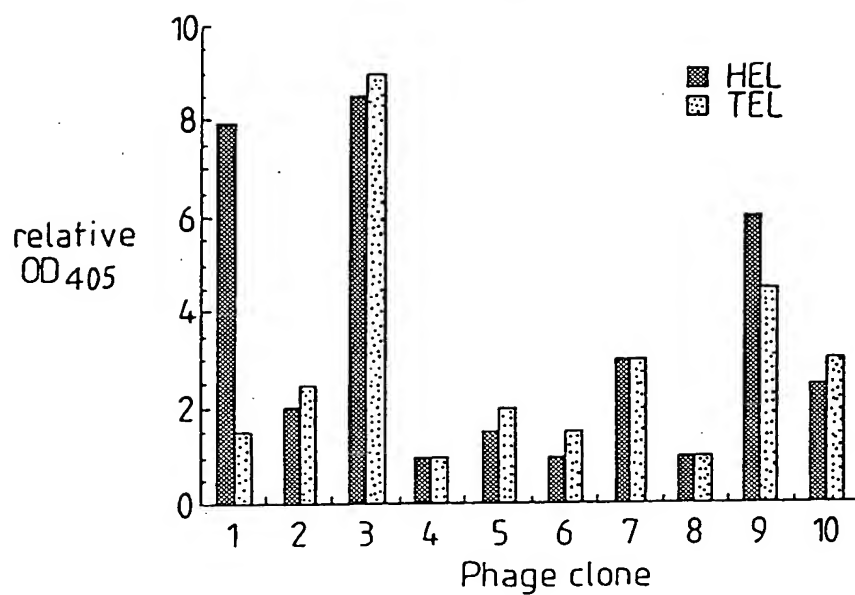


Fig.53.

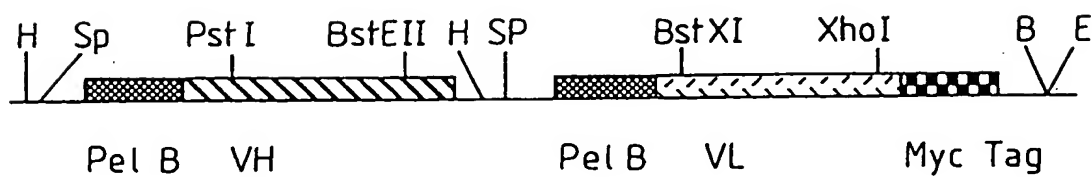


Fig.52.

CDR 1

CDR 2

D1.3 DIQMTQSPASLSASVGETVTITCRASGNIHNYLA WYQQKQKSPQLLVYYTTTLD
M1F DIELTQSPSSLSASLGERVSLTCRASQDIGSSLN WLQQEPDGTIKRLIYATSSLDS
M21 DIELTQSPALMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLAS

CDR 3

D1.3 GVPFRFSGSGGTQYSLKINSLQPEDFGSYQCQHFWSPTPTFGGGTKLEIKR
M1F GVPKRFSGSRGSDYSLTISSLESEDFVDYVCLQYASSPWTFFGGGKLELKR
M21 GVPVRFSGSGGTSYSLTISSMEAEADAATYQCQWSSYPPLTFGAGTKLEIKR